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OM protein - protein search, using sw model

Run on:

October 29, 2002, 03:48:42; Search time 25 Seconds (without alignments) 535.879 Million cell updates/sec

US-09-886-041-2 1853 1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH 346 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 segs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scription	P49019 homo sapien 000270 homo sapien 092031 mus musculu 091875 homo sapien 14996 gallus muscullu gallus muscullu gallus muscullu gallus muscullu gallus muscullu gallus muscullus gallus muscullus gallus gall
SUMMARIES	HM74_HUMAN GPRV_HUMAN GPRV_HUMAN CLT72_HUMAN P27R_CHICR P27R_BOVIN CLT72_PIG P27R_BOVIN CLT72_PIG P27R_BOVIN CLT72_PIG P27R_BOVIN CLT72_PIG P27R_BOVIN CLT72_PIG P27R_BOUSE P27S_HUMAN P27S_CHICR GPRE_HUMAN P27S_HUMAN
DB	
Length	387 387 387 387 387 387 387 387 387 387
& Query Match	7.47.00.00.00.00.00.00.00.00.00.00.00.00.00
Score	306.5 307.5 306.5 306.5 306.5 306.5 306.5 336.5 36.5
Result No.	22 4 4 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

P30680 rattus norv Q63371 rattus norv P30937 rattus norv P30935 mus musculu P34994 sus scrofa P31391 homo saplen Q63645 rattus norv P32745 homo saplen P26824 rattus norv Q971k6 mus musculu P30936 rattus norv	
SSR2_RAT P2Y6_RAT SSR4_RAT SSR3_MOUSE SSR3_PIG SSR4_HUMAN PAR2_RAT SSR3_HUMAN THRR_RAT GPRY_MOUSE SSR3_RAT	PAR2_HUMAN
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369 3269 3368 3369 3397 4418 4322 428	397
100 100 100 100 100 100 100 100 100 100	16.0
3000 2000 2000 2000 2000 2000 2000 2000	297
333334 4444 4444 432 433 443 443 443	45

## ALIGNMENTS

				. 500			
	HM74_HUMAN	STA	STANDARD;	PRI;	387	AA.	
	P49019; 01-FEB-1996	(86)		Created			
	01-FEB-1996	(Rel.		sequence update)	updat	(e)	
	16-0CT-2001	(Rel.	40, Last		pdn u	ate)	
	Probable G	protein	protein-coupled	receptor HM74	HM74.		
	HM/4.		•				
	Fultariota (numan)	Moterone.	ni). . Chordata.		, d+	Graniata: Vortobrata: Futolo	Putolocatom:
36	Mammalia.	Furtheria:			hini.		(TIII)
		9606:				7000	
	[1]	)					
	SEQUENCE FROM N.A.	ROM N.A.					
	TISSUE-Monocytes;	cytes;					
	MEDLINE-94	192629;	PubMed-7	505609;			
	Nomura H., Nielsen	Nielsen	B.W., P	B.W., Matsushima K.;	ж.,,		
	"Molecular	cloning	of cDNAs	s encoding	aLD	a LD78 receptor and putative	utative
	leukocyte	shemotac	ttc pept	ide recept	ors."		
	Int. Immunol. 5:1239-1249(1993).	1. 5:12	39-1249(	1993).			
	· NOTTONIE	IN. ORDE	ORDHAN RECEDIOR	. ACT			
		TI AP II	T ATTOM.	Totogral a	ardmo	CHROTILITAD IOCATION: Integral membrane protein	
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	HSSP; P349	16; 10DL					
	GCKUD; GCK_U328;						
-	MIM; 60603						
	InterPro; IPR000276; GPCR_Rhodpsn.	FE00027	6; GPCR	Rhodpsn.			
	Pfam; PF00(	301; 7tm	, ,				
	PROSITE; P	PS00237;	G_PROTE	G_PROTEIN_RECEP_F1_1;	1, 1	•	
	PROSITE; P:	350262;	G_PROTE	N_RECEP_F1	2; 1.	;	
KW	G-protein	coupled	receptor;	; Transmembrane	brane		
FT		, <del>, ,</del>	28	EXTRACELLULAR	LLULA	R (POTENTIAL).	
FI	TRANSMEM	29	20	1 (POTENTIAL)	NTIAL		
	DOMAIN	51	63	CYTOPLA	SMIC	CYTOPLASMIC (POTENTIAL).	
_	TRANSMEM	64	85	2 (POTE	(POTENTIAL)		
	DOMATN	9 6	102		T.T.II.A	A POTENTIAL)	
_	TRANSMEM	103	123	3 (POTENTIAL)	NTIAL		
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                                                                                                                                                                                                                                                             FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
                                                                                                                                                                                                                                                                                                                                                                                                                  MICLPFRIDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                                                                                                                                                                                                                                                                 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
                                                                                                                     Gaps
                                                                                                                                                         5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
                                                                                                                                                                                encoding a putative G protein-coupled receptor.";
Genomics 42:519-523(1997).
Genomics 42:519-523(1997).
Genomics 42:519-523(1997).
Genomics 42:519-523(1997).
Genomics 52:519-523(1997).
Genomics 52:519-523(1997)
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G., Santoni A.,
                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and chromosomal localization of GPR31, a human gene
                                                                              Length 387;
                                                                                                                     Indels
                        C244F562C2343647 CRC64;
    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 KOPGHSKTORPEEMPISNLGRRSCISVANSFOSOSDGOWDP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2ingoni A., Rocchi M., Storiazzi C.T., Bernardini
Napolitano M.;
                                                                            5%; Score 880.5; DB 1; 2%; Pred. No. 1.1e-54; 49; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probable G protein-coupled receptor GPR31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 AA
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Last annotation update
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                      BY
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(Rel. 36, Last sequ
(Rel. 40, Last anno
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PRINTS; PR00237; GPCRRHODOPSN.
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Mammalia; Eutheria; Primates;
                                          44481 MW;
                                                                            47.5%;
52.2%;
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                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
299 3
100 1
387 AA;
                                                                                                 Similarity
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16-OCT-2001
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                                                                                                                   Matches 178;
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000270;
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                                                                              Query Match
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Hui Y., Yang G., Galczenski H., Figueroa D.J., Austin C.P.,
Copeland N.G., Gilbert D.J., Jenkins N.A., Furk C.D.;
Copeland N.G., Gilbert D.J., Jenkins N.A., Furk C.D.;
Copeland N.G., Gilbert D.J., Jenkins C.C.,
Genomic cloning, alternative splicing, and in vitro
characterization.";
J. Biol. Chem. 276:47489-47495(2001).
-I- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-
calcium second messenger system. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :: :|| :|| || || || || || CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVVNDVVYCFSSPTFRSSYRRV
                                                   1 (POTENTIAL).
CYPODESMIAL).
CYPODESMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                  7A4F164CD9C969DD CRC64;
                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         121;
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                                                                     7 (POTENTIAL).
CYTOPLASMIC (POT)
N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cysteinyl leuveriene receptor 2 (CystIR2).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Mismatches
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                                                                                                                                                      3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                  24.2%; Score 448.5; 34.0%; Pred. No. 1.1
                                                                                                                                                                                        4 (POTENTIAL)
G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
                 OSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1. protein coupled receptor; Transmembrane.
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1180
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PubMed=11591709;
                                                                                                                                                                      111
132
153
181
202
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53
74
92
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sapiens (Human)
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                                                                                           Usage by and for commercial
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QNS75; Q9HCQ2;

Q1-MAR-2002 (Rel. 41, Created)

Q1-MAR-2002 (Rel. 41, Last sequence update)

Q1-MAR-2002 (Rel. 41, Last annotation update)

Cysteinyl leukotriene receptor 2 (CysLTR2) (PSEC0146) (HG57) (HPN321).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 LIMNHIAVAVGFLLPPLTLTVCYLLIIRILLKAEIPESGPRAAHRKALTTIVIAMITFLL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                          59 VADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 HPHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC-----ESFIMESA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 NGWHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFIT 231
       TISSUE SPECIFICITY: Widely expressed at low levels, with highest expression in the spleen, thymus and adrenal gland, and lower in the kidney, brain and peripheral blood leukocytes. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                     2 YNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLA 58
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                       LINKED (GLCNAC. . .) (POTENTIAL). 327B14A6EDDD2A02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 CYLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 309;
                                                                                                                    Indels
                                                                                                                                                                                                               2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                              1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                            7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed at low leve
                                                                                                                                                                                                                                                                                                                                                                 20.0%; Score 371.5; DB 1; 32.7%; Pred. No. 2.5e-19; ive 56; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC.
                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                 35227 MW;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                              47
56
77
77
98
1119
1138
1187
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309
171
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95
14
309 AA;
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   .96
                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
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MEDLINE-20459128; PubMed-10851239;
Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
Lynch K.R., Evans J.F.,
"Characterization of the human cysteinyl leukotriene 2 receptor.";
J. Biol. Chem. 275:30531-30536(2000).
                                                                                                                                                                                                                                                                                          "The molecular characterization and tissue distribution of the human
                                                                                                                                                                                               Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T
Nishikawa T., Kawai Y., Masuho Y., Isogai T., Suzuki Y., Sugano S.,
Furuichi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and characterization of a second human cysteinyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukotriene receptor: discovery of a subtype selective agonist."; Mol. Pharmacol. 58:1601-1608(2000).
   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
                           Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn M.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
   Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                        cysteinyl leukotriene CysLT2 receptor.";
Biochem. Biophys. Res. Commun. 274:316-322(2000)
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InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                             SEQUENCE FROM N.A.
TISSUE-Placenta;
MEDLINE-20374466; PubMed-10913337;
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   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB041644; BAB16379.1; -
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PRINTS; PR01533; CYSLTRECPTR.
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                                                      NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC---ESFIMESANGW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFITCYL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 NSRNCTIE-NFKREFFFIVYLIIFFWGVLGNGLSIYVF---LQPYKKSTSVNVFMLNLAI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69; Mismatches 134; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 NGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST----VYLFNLAV 59
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 346;
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                     4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                              2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 366.5;
Pred. No. 6.1
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MEDLINE-93285340; PubMed-8508924;
                                                                                                                                                                                                                                                                                                                                                                                                                                         39635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.8%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         346 AA;
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Best Local Similarity
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P34996;
                                                                                            TRANSMEM
DOMAIN
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TRANSMEM
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TRANSMEM
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between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PDB; 11-JUL-96.
GCRDb; 11-JUL-96.
GCRDb; 11-JUL-96.
InterPro; IPR00027; GPCR_Rhodpsn.
PRINTS; PR00237; GPRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58; Mismatches 130; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
Webb T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G.,
King B.F., Burnstock G., Barnard E.A.;
"Cloning and functional expression of a brain G-protein-coupled ATP
                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMILL
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 9.5e-19;
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                                                                         FEBS Lett. 324:219-225(1993).
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Best Local Similarity 29.1:
Matches 95; Conservative
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362
191
                                                                                                                      3D-STRUCTURE MODELING
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P2YR_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                          138 TLWALVIL------GTVYLLLENHLCVQETA-----VSCESFIMESANGWHD 178
                                                                                                                                                                   ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor) (6H1 orphan receptor).
                                     163 LVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFM-----
                                                                               179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE=94335907; PubMed=8058061;
Filtz T.M., Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
"Expression of a cloned P2Y purinergic receptor that couples to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIMIS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                         362 AA.
                                                                                                                                                                                                                                                     292 LKICSLKPKQPGHSKTQRPEEMPISNL 318
                                                                                                                                                                                                                                                                                  | : :| : :| :: |
| 327 ATRKSSRRSEP--NVQSKSEEMTLNIL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Pharmacol. 46:8-14(1994).
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HSSP; P34996; 1DDD.
GCRDb; GCR_2392;
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P49652;
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TLWALVIL------GTVYLLLENHLCVQETA------VSCESFIMESANGWHD 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 LVWALVVAVIAPILFYSGTGVRNKTITCYDTTADEYLRSYFVYSMCTTVFM----- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                         4 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

5 (POTENTIAL).

CYPOLASHIAL).

6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASHIAL).

CYTOPLASHIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP---
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TISSUE-Acrtic endothelium;
MEDLINE-95352058; PubMed-7626079;
Mederson D.J., Elliot D.G., Smith G.M., Webb T.E., Dainty I.A.;
"Cloning and characterisation of a bovine P2Y receptor.";
Blochem. Blophys. Res. Commun. 212:648-656(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2VI) (Purinergic receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                   19.6%; Score 364; DB 1; Length 362; 29.1%; Pred. No. 9.5e-19;
               1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Mismatches 130; Indels
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                               41180 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                  11
26
102
186
362 AA;
   P2YR_BOVIN
                                                     TRANSMEM
DOMAIN
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TRANSMEM
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TRANSMEM
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288 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corpus callosum.";
Neurobiol. Dis. 5:259-270(1998).
-I- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                     Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.; "Cloning and expression of a P2y purinoceptor from the adult bovine
                                                                                          ATP AND ADP.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.6%; Score 362.5; DB 1; Length 373; 27.5%; Pred. No. 1.2e-18; tive 68; Mismatches 140; Indels 35.
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2 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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PROSITE; PS00237; G_PROTEIN_RECEP_FI_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
TRANSMEM 53 74 I (POTENTIAL).
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CYTOPLASMIC (PO
BY SIMILARITY.
                                                                                                                                                                                                                                                                        InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.
SEQUENCE FROM N.A.
TISSUE-Corpus callosum;
MEDLINE-99064562; Pubmed-9848096;
                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42287 MW;
                                                                                                                                                                                                                                                  EMBL; U34041; AAC78275.1; -. HSSP; P34996; 1DDD.
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373 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of the cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
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(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-protein coupled receptor; Transmembrane; Glycoprotein. DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB052662; BAB60817.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PEdm; PF000001; 7tml; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.5%; Score 362; DB 1;
                                                                                                                                                                         QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
                                        --ATRKASRRSEANLQSKSEDMTLNILSEFKONGD 370
                                                                                                                                                  345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
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31.3%; Pro-
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308
345
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177
184
345 AA;
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
DISULFID
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TRANSMEM
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PRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phis SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                           LFCSFKIVWSLRRRQQLARQARM--KKATRFIMVVAIVFITCYLPSYSARLYFLWTVPSS 250
                                         LRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGI 135
                                                                                136 VCTLWALVILGTVYLLLENHLCVQETAVSC---ESFIMESANGWHDIMFQLEFFMPLGII 192
                                                                                                                                            219 SICYLLIIRALLKVEVPESGLRLSHRKALITVIIALIIFLLCFLPYHVLRTLHLLEWKAD 278
                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                    66
             PPLLIVAFVLGALGNGVALCGFCFHMKTWKPST - - - VYLFNLAVADFLLMICLPFRTDYY
                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
P2r purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; It.

PRINTS; PRO0237; GPCRHODOPSN.

PROSTTE; PRO0237; G_PROTEIN_RECEP_F1_1; 1.

PROSTTE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSTTE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_PROTEIN COUPLED RECEP_F1_2; 1.

FEXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                             251 ACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                          373 AA.
                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U22830; AAA91303.1; -.
                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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74
87
109
147
166
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        P2YR_RAT
P49651;
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Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of the cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STORTH STATE STATE STATE STATE STATES STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 LVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSM-----CTTVAMFCI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYFLWTVPSSACD -- PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDF---QTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR----- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLWALVILGTVYLLLENHLCVQET-AVSC------ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptors.";
Submitted (Dec-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
-!- SUBCELULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                            EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

RY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP----SVSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 2 (CysLTR2) (RSBPT32).
CYSLTR2 OR CYSLT2.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.3%; Score 358.5; DB 1; 27.0%; Pred. No. 2.3e-18; tive 68; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 PKQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ATRKASRRSEANLOSKSEEMTLNILSEFKONGD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42321 MW;
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hes 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        113
197
373 AA;
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1167
239
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2266
2304
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Q924T9;
                                        DOMAIN
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 HPHHAVNTISTRVAAGIVC-TLWALVILGTVYLLLENHLCVQETAVSCESFIMESAN--G 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 VADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 WHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFITCY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
bustrychai Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.

N-LINKED (GLGNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

A122AC8177879D56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2X1) (Purinergic receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 LPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                        19.2%; Score 355.5; DB 1; Length 3(31.2%; Pred. No. 3.2e-18;
tive 57; Mismatches 131; Indels
                                                     EMBL; AB052661; BAB60816.1; -.
EMBL; AB052661; BAB60816.1; -.
PitterPro: TFM00021; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
26 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                         2 (POTENTIAL).
EXTRACELLUAR (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
EXTRACELUAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                 1 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                               35507
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Matches 91; Conservative
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166 1
167 1
309 AA;
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SEQUENCE FROM N.A.
TISSUE-Placenta;
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P47900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular basis for ADP-induced platelet activation. II. The P2X1
"Molecular basis for ADP-induced platelet activation. II. The P2X1
"Molecular basis for ADP-induced platelet activation. II. The P2X1
"receptor mediates ADP-induced intracellular calcium mobilization and receptor mediates ADP-induced intracellular calcium mobilization and a shape change in platelets."

"Biol. Chem. 273:2030-2034(1998).

"In Sincerior for Extracellular ADP LEADS TO MOBILIZATION OF INTRACELLULAR CALCIUM IONS VIA ACTIVATION OF PHOSPHOLIPASE C, A CHANGE IN PLATELET SHAPE, AND PROBABLY TO PLATELET AGGREGATION.

"CHANGE IN PLATELET SHAPE, AND PROBABLY TO PLATELET AGGREGATION."
"INDUCTION: REPRESSED BY THE P2X1 RECEPTOR-SPECIFIC ANTAGONISTS A3P5PS, A3P5P AND A2P5P. THESE INHIBIT CALCIUM ION MOBILIZATION OF AND SHAPE CHANGE IN PLATELETS.

"AND SHAPE CHANGE IN PLATELETS."

"CHANGE IN PLATELETS."
                                                                                                                                                                                      Ayyanathan K., Tania W., Harbansjit S., Raghbir A.S., Barnard E.A.,
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Pfam; PF00001; 7tm_1; 1.
PRNTNS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPOTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;
MEDLINE-96257237; PubMed-8666290;
Leon C., Vial C., Cazenave J.-P., Gachet C.;
"Cloning and sequencing of a human cDNA encoding endothelial P2Y1
                                                                                                                                                                                                                                                                                                                                                                                      Janssens R., Communi D., Pirotton S., Samson M., Parmentier M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and tissue distribution of the human P2X1 receptor."; Biochem. Biophys. Res. Commun. 221:588-593(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leon C., Vial C., Weber J., Cazenave J.-P., Gacher C.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   Kunapuli S.P.; "Cloning and chromosomal localization of the human P2Y1
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1 (POTENTIAL).
                                                                                                                                                                                                                                                                purinoceptor.";
Biochem. Biophys. Res. Commun. 218:783-788(1996).
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                                                                       purinoceptor.";
Gene 171:295-297(1996).
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MEDLINE-95298025; PubMed-7779087;
MEDLINE-95298025; PubMed-7779087;
TOkuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
"Cloning of rat and mouse P2Y purinoceptors.";
"Cloning of rat and mouse P2Y purinoceptors.";
Blochem. Blophys. Res. Commun. 211:211-218(1995).
-1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS OF EXTRACELLULAR ATP ON INSULIN SECRETION.
                                                                                                                                                                                                                                                                    174 LVWLIVVVAISPILEYSGEGVRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228
                                                                                                                                                                                                                                                                                                                                           RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                            TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
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                                                                                                                                                                                                                                                                                                                                PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP----SVSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                 (GLCNAC. ..) (POTENTIAL).
(GLCNAC. ..) (POTENTIAL).
(GLCNAC. ..) (POTENTIAL).
                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
                                                                                                                                                                                                         28;
                                                                                                                                                                                   ; DB 1; Length 373;
4.8e-18;
                                                                                                                                                                                                       66; Mismatches 132; Indels
                                                                                       EXTRACELLULAR (POTENTIAL).
                  EXTRACELLULAR (POTENTIAL)
                                           4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                    CYTOPLASMIC (POTENTIAL).
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 CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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les 93; Conserv
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P2YR_MOUSE
P49650;
 DOMAIN
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P2YR_MOUSE
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                              -i - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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2 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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MGD; MGI:105049; P2ryl.
InterPro; IPR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1, 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein couple receptor; Transmembrane; Glycoprotein.
DOMAIN.

1 52 EXTRACELLULAR (POTENTAL).
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SUBCELLULAR LOCATION: Integral membrane protein
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; Mismatches 143;
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-97366605; PubMed-9223435;
Janssens R., Boeynaems J.M., Godart M., Communi D.;
"Cloning of a human heptahelical receptor closely related to the P2Y5
                                                                      9) (G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: NOT DETECTED IN THE BRAIN REGIONS THALAMUS,
PUTAMEN, CAUDATE, FRONTAL CORTEX, PONS, HYPOTHALAMUS, HIPPOCAMPI
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                             MEDLINE-97225799; PubMed-9073069; O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q., Kolakowski L.F. Jr., Lynch K.R., George S.R.; "Cloning and chromosomal mapping of four putative novel human Gene 187:75-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PR0SITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PR0SITE: PS050263; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Bohm S.K., Khitin L.M., Payan D.P., Bunnett N.W.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 236:106-112(1997)
                                 16-OCT-2001 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P2Y purinoceptor 9 (P2Y9) (Purinergic receptor GPR23) (P2X5-11ke receptor).
          370 AA.
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U66578; AAC51301.1; -.
EMBL; U90323; AAB62087.1; -.
EMBL; U90322; AAB62088.1; -.
EMBL; AF005419; AAB66322.1; -.
HSSP; P34996; 1DDD.
GCRDb; GCR_1323; -.
GCRDb; GCR_1324; -.
GCRDb; GCR_1324; -.
GCRDb; GCR_1324; -.
MIM; 300086; -.
        P2Y9_HUMAN STANDARD; 099677; 015132; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last seq
                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                            NCBI_TaxID=9606;
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65
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                    GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKLKICSLKPKQPGHSK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 VILGTVYLLLENHLCVQETAVSC-ESFIMESANGWHDIMFQLE------FFMPLGIILF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaplan M.H., Smith D.I., Sundick R.S.;
"Identification of a G protein coupled receptor induced in activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T cells.";
J. Immunol. 151:628-636(1993).

- Immunol. 151:628-636(1993).

- SUBCELLULAR LOCATION: Integral membrane protein.

- SUBCELLULAR LOCATION: INDUCED IN ACTIVATED T-CELLS.

- TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.

- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                    BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

F -> L (IN REF. 3).

W; 20857F52A3929E48 CRC64;
                                                                                                                                                                                                                                                                                                                        VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 CSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 VLSGGISASLFSTTNVNNATTTCFEGF -- - SKRVWKTYLSKITIFIEVVGFIIPLILNVS
                                                                                                                                                                                                                       18.7%; Score 346.5; DB 1; Length 370; 31.2%; Pred. No. 1.6e-17; Live 52; Mismatches 128; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
P2Y purinoceptor 5 (P2Y5) (Purinergic receptor 5) (6H1).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                         41895 MW;
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                                                                                                                                                                                                                                                                        Conservative
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111
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370 AA;
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P2Y5_CHICK
ID P2Y5_CHICK
AC P32250;
                                                                                                                                                                                                                                                                     95;
                                                                                                                     CARBOHYD
CONFLICT
SEQUENCE
                         DISULFID
CARBOHYD
                                                                          CARBOHYD
                                                                                                 CARBOHYD
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MIM; 603071;
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                                                                 Premi Pronoform Control of Contro
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MEDILED-96145150; Pubmed-8558062;
Raport C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,
Godiska R., Gray P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC-TLWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 VILGTV---YLLLENHLCVQETAVSCESFIMESANGWHDIMFQL------EFFMPLGII 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 VLAGSTPASFFQSTNRQNNTEQRICFENF -- - PESTWKTYLSRIVIFIEIVGFFIPLILN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFCSFKIVWSLRRQQLAR-QARMKKATRFIMVVAIVFITCYLP-SVSARLYFLW---TV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPKQPGHSKT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRHWAF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                             4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

8 PALINKED (GLCNAC, ...) (POTENTIAL).

PALINKED (GLCNAC, ...) (POTENTIAL).

PALINKED (GLCNAC, ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.3%; Score 339; DB 1; Length 30 30.3%; Pred. No. 4.5e-17; Live 56; Mismatches 123; Indels
                                                                                                                                                                                                                                                                     1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                  3 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40) Last annotation update)
Putative G protein-coupled receptor GPRI7 (R12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 AA
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HSSP; P34996; 1DDD.
SCRDb; GCR_0689; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35597 MW;
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308 AA;
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131
152
179
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Q13304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                     Palmitate.
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ģ
                                                                              67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGQETPLENMLFASFYLLDFILALVGNTLALMLFIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYPOLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

8Y SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BD2AEDB2FEBF15E1 CRC64;
ww members of the chemokine receptor gene family.";
Leukoc. Biol. 59:18-23(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37826 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 033447; AAB16746.1; -. EMBL; 294154; CAB08107.1; -. HSSP; P34996; 1DDD. GCRD; GCRL 1968; -. GCRD; GCR_2597; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                          SEQUENCE FROM N.A.
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169
196
217
233
254
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ð qq

Qy Dp

<sup>299</sup> PKQPGHSKTQRPEEMPIS 316 | | | | | | 317 1KGPPPSFEGKTNESSLS 334

Search completed: October 29, 2002, 04:52:57 Job time : 27 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

October 29, 2002, 04:51:26 Run on:

; Search time 44 Seconds
(without alignments)
755.612 Million cell updates/sec

US-09-886-041-2

1853 1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH 346 Perfect score: Sequence:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_71:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	G protein-coupled	G protein-coupled	P2Y receptor - bov	G protein-coupled	heptahelical P2Y5-	G protein-coupled	intron 17 purinerg	ATP receptor P2u -	thrombin receptor	somatostatin recep	somatostatin recep	somatostatin recep	somatostatin recep	angiotensin II rec	somatostatin recep	bradykinin B2 rece	proteinase activat	somatostatin recep	somatostatin recep	G protein-coupled	brain-specific som	somatostatin recep	somatostatin recep	somatostatin recep	somatostatin recep	thrombin receptor	probable G protein	proteinase-activat	somatostatin recep
SUMMAKIES	ΩI	169202	S33733	JC4162	JC4737	JC5549	150241	T09508	A47556	151667	157940	C41795	A41795	A39297	S15403	B41795	JQ1488	148705	A45291	D41795	I55450	A47249	A44021	JC2083	JN0605	A46226	A43448	830508	S66518	S29248
	80	8	~		~	~	~	7	7	~	7	7	7	7	7	~	•	~						7		•	•		7	7
	Query Match Length	387	362	373	373	370	308	344	373	420	363	391	391	391	359	369	364	399	369	369	328	384	428	369	388	418	432	428	397	346
æ	Query Match	47.5	19.6	19.6	19.1	18.5	18.3	17.5	17.3	16.8	16.7	16.6	16.5	16.5	16.4	16.3	16.3	16.3	16.2	16.2	16.2	16.2	16.2	16.2	16.1	16.1	16.1	16.1	16.0	16.0
	Score	880.5	364	362.5	354	343.5	339	324	320	310.5	309.5	307	305.5	305.5	304.5	302.5	302	302	300.5	300.5	300	300	300	299.5	599	298.5	298.5	298		296.5
	Result No.	1	7	e	4	S	9	7	œ	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29

S33733 G protein-coupled receptor - chicken C;Species: Gallus gallus (chicken)

RESULT 2

angiotensin II rec P-2U nucleotide re	somatostatin recep	G protein-coupled	G protein-coupled	anglotensin II rec	angiotensin II rec	delta opioid recep	angiotensin II rec	chemokine (C-C) re	delta opioid recep	G protein-coupled	probable chemoattr	angiotensin II rec	allatostatin recep
A48857 A54946	JC4629	JC5653	JC5498	S44425	JC2134	S34592	JC1104	A45177	B48227	S68208	JC5796	JH0621	JC7677
00	7 17	9 (7	7	~	7	7	~	~	~	7	7	~	7
359	384	361	371	359	359	372	359	355	372	365	371	359	423
16.0	15.9	15.8	15.8	15.7	15.7	15.7	15.6	15.5	15.5	15.5	15.5	15.5	15.5
296 296	295	292.5	292	291.5	291.5	290	289	288	288	287.5	287.5	286.5	286.5
30	32	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
G protein-coupled receptor HM74 - human
C;Species: Homo sapiens (man)
C;Accession: 169202
R;Nomura, H; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte c
A;Reference number: 154751; MUID:94092629
A;Reference number: 154751; MUID:94092629
A;Accession: 169202
A;Accession: 169202
A;Accession: 169203
A;Accession: Iffar cRES>
A;Corsor references: GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867
C;Genetics:
A;Construct
C;Genetics:
A;Construct
C;Superfamily: G protein-coupled receptor 4
                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 SCCRIEGDIISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                     Length 387;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
                                                                                                                                                                                                                                                                                                                                                 47.5%; Score 880.5; DB 2; 52.2%; Pred. No. 5.1e-74; tive 49; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.2%
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316
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                                                                T.G.; King, B.F.; Burnstoc
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F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
                                                     Riwebb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burns, FEBS Lett., 324, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor. A; Accession: S33733
A;Steference number: S33733
A;Accession: S33733
A;MUD:93285340
A;Accession: S32733
A;Mulecule type: mRNA
A;Molecule Lype: mRNA
A;Residues: 1-362 <WEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: S33733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Bos primigenius taurus (cattle)
Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                    A;Residues: 1-362 <WEB>
A;Cross-references: EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395085
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLWALVIL------GTVYLLLENHLCVQETA------VSCESFIMESANGWHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP--- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 LVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFM----- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Bos primity......
C.Date: 12-Oct-1995 #sequence_revision lu-mov.
C.Date: 12-Oct-1995 #sequence_revision lu-mov.
C.Accession: JC4162
R.Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Blochem: Blophys. Res. Commun. 212, 648-656, 1995
A;Title: Clonding and characterisation of a bovine P2Y receptor.
A;Reference number: JC4162; MUID:95352058
A;Accession: JC4162
A;Accession: JC4162
                                                                                                                                                                                                                                                                                                                                                                                     19.6%; Score 364; DB 2; Length 362; 29.1%; Pred. No. 4.6e-26; Live 58; Mismatches 130; Indels
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C. Superfamily: ATP receptor P2u
C. Seywords: glycoprotein; phosphoprotein; receptor; transme
F; 52-77/Domain: transmembrane #status predicted <TM1>
F; 124-150/Domain: transmembrane #status predicted <TM2>
F; 171-191/Domain: transmembrane #status predicted <TM4>
F; 214-237/Domain: transmembrane #status predicted <TM5>
F; 51-282/Domain: transmembrane #status predicted <TM5>
F; 305-328/Domain: transmembrane #status predicted <TM5>
F; 11, 27, 113, 197/Binding site: carbohydrate (ASN) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 LKICSLKPKQPGHSKTQRPEEMPISNL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 ATRKSSRRSEP--NVQSKSEEMTLNIL 351
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                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 95; Conserv
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Length 373;

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Grafian coupled receptor P2X1 - human
N.Alternate names: P2X1 purinergic receptor; P2X1 purinoceptor
C.Species: Howo sapiens (man)
N.Alternate names: P2X1 purinergic receptor; P2X1 purinoceptor
C.Species: Howo sapiens (man)
C.Date: 10-May-1996 #text_change 17-Nov-2000
C.Caccesion: UG/737; UG/615; S54253
R.Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M
Blochen Blophys. Res. Commun. 221, 588-593, 1996
A.Title: Cloning and tissue distribution of the human P2X1 receptor.
A;Reference number: J373 cdAX7
A;Molecule type: DNA
A;Residues: 1-373 cdAX7
A;Molecule type: DNA
A;Residues: 1-373 cdAX7
A;Molecule type: NBA
A;Title: Cloning and chromosomal localization of the human P2X1 purinoceptor.
A;Reference number: JC4615; MUID:96158962
A;Title: Cloning and chromosomal localization of the human P2X1 purinoceptor.
A;Reference number: JC4615; MUID:96158962
A;Title: Cloning and chromosomal localization of the human P2X1 purinoceptor.
A;Reference number: JC4615
A;Molecule type: MRA
A;Residues: 1-373 cdAY7
A;Cross-references: GB:U42029; NID:91147730; PIDN:AA97872.1; PID:91147731
A;Residues: 1-373 cdAY2
A;Cross-reference number: S54253
A;Accession: GC-7 Vala.
A;Residues: 1-373 cdAY2
A;Accession: S4223
A;Accession: Gloning of a human putative P2Y receptor.
A;Residues: 1-137,139-373 clED>
A;Residues: 1-137,139-373 clED>
A;Residues: 1-137,139-373 clED>
A;Residues: 1-137,139-373 clED>
A;Generic comment: This receptor belongs to a family of G protein-coupled receptors. It responses content of the mRA
A;Generic content of the mRA
A;Generic content cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/Gene: P271; GDB:P2RV1
A/Cross-references: GDB:677125; OMIN:601167
A/Cross-references: GDB:677125; OMIN:601167
C/Superfamily: ATP receptor P2u
C/Superfamily:
                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----SVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                        Gaps
                                                                                                                                                                                       18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                 Indels
                                                                 Mismatches 140;
      Pred. No. 6.6e-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- ATRKASRRSEANLQSKSEDMTLNILSEFKQNGD 370
                                                          68;
27.5%;
      Best Local Similarity 27.5
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288
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                                                          Matches
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cells

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activated T
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C;Species: Gallus gallus (chicken)
B;Rcession: I50241; UC4618
B;Raplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Fitle: Identification of a G protein coupled receptor induced in activated
A;Reference number: I50241; MUID:93329058
            : || || RMESLFKT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC-TLWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 VILGTV---YLLLENHLCVQETAVSCESFIMESANGWHDIMFQL------EFFMPLGII 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-308 cKAR>
A.Residues: 1-308 cKAR>
A.Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
R.Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
B.Jochem: Biophys: Res. Commun. 219, 105-110, 1996
A.Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A.Reference number: JC4618; MJID:96190677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPKQPGHSKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; A;Experimental source: T-cells C;Comment: This receptor plays a role in T-cell activation.
            A connection of the property of the product of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSDTNSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.3%; Score 339; DB 2; 30.3%; Pred. No. 8.1e-24;
                                                                                                                                                                                                                                                                                                                     chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                     protein-coupled receptor
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Best Local Similarity
Matches 91; Conserv
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A; Residues: 1-308 <WEB>
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                                                                                                 308 QRP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
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                                         282
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F;261-282/Domain: transmembrane #status predicted <TW6>
F;305-328/Domain: transmembrane #status predicted <TW7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict
F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict
F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999
C; Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999
C; Accession: JC5549
R; Janssens, R: Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Blophys. Res. Commun. 236, 106-112, 1997
A; Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A; Reference number: JC5549; MUID: 97366605
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A;Residues: 1-370 <JAN>
A;Cross-references: DDBJ:AF005419; NID:g2240034; PIDN:AAB66322.1; PID:g2240035
C;Superfamily: ATP receptor P2u
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                                                                                                                                                                                                                                                                                                                                                                              TLWALVILGTVYLLLENHLCVQET-AVSC------ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 VVFILGLITUSVSLFVFCFRAKRRSETAIFITULAVSDLFVCTLPFKI-FYNFNRHWPF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 VILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE-----FFMPLGIILFC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKLKICSLKPKQPGHSKT 307
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                                                                                                                                                                                                                                                                                                                                           18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 LVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || :|| | || :| : | : :| || :| || PLVLILGCYGLIVRALIXK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 VLSGGISASLFSTTNVNNATTTC -- FEGLSKRVWKTYLSKITIFIEVVGFIIPLILNVSC
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                                                                                                                                                                                                                      DB 2; Length 373;
                                                                                                                                                                                                                                                                                  66; Mismatches 132; Indels
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Pred. No. 3.8e-24;
                                                                                                                                                                                                                                                         4e-25;
                                                                                                                                                                                                                      19.1%; Score 354; 29.2%; Pred. No. 4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heptahelical P2Y5-like receptor - human
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1 Similarity 31.0%;
94; Conservative 5
                                                                                                                                                                                                                                                   Similarity 29.2
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: JC5549
                                                                                                                                                                                                                                Local Sim.
                                                                                                                                                                                                                      Query Match
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Matches
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Intron 17 purinergic receptor P2Y5 - human N'Alternate names: G-protein coupled receptor C;Species: Homo sapiens (man) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999 C;Accession: T09508 R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W. submitted to the EMBL Data Library, April 1997 A;Description: The human purinergic receptor P2X5 is encoded in intron 17 of the retinob A;Reference number: 216705 A;Accession: T09508 A;Accession: T09508 A;Accession: A;Wolecule type: mRNA A;Residues: 1-344 <boh> A;Cossion: Experiments of the Complex of the Complex</boh>	Qy 124 VNTISTRVAAGIVCA Db 142 LRWGRARYARNAAN Qy 175 GWHDIMFQLEFFRPL Db 201VMLGLLFAVER Qy 227 IVFITCYLP-SVGAN Db 252 AVFALCELFFHVFRI Qy 284 SFPKFYNKLKICSLR Qy 284 SFPKFYNKLKICSLR Db 312 RLVRFARDAK	VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESAN 174  L.     :       :       :
C; Superforming: Air leceptor Figure C; Keywords: G protein-coupled receptor; transmembrane protein Query Match 17.5%, Score 324; DB 2; Length 344; Best Local Similarity 30.8%; Pred. No. 2.3e-22; Matches 88; Conservative 56; Mismatches 120; Indels 22; Gaps 10;	RESULT 9 151667 thrombin receptor - Afril C;Species: Xenopus laevi	
OY 24 VAFVLGALGNGVALCGECFHMKTWKPSTVYLFNLAVADFLLMICLPFRIDYYLRRHWAF 83  1	C;Date: 13-Sep-1996 #sequence_revision 13-Sep-19 C;Accession: 151667 R;Gerszten, R.E.; Chen, U.; Ishii, M.; Ishii, K. Nature 368, 648-651, 1994 A;Title: Thrombin recepeor's specificity for ago	uence_revision 13-Sep-1996 #text_change 21-Ju1-2000 J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H. 4 or's specificity for agonist peptide is determined by its ext 67; MUID:94195429
LAIVYPFKS-KTLRTKRNAK SANGWHDIMFQLEI : : : : ATWKTYLSRIVIFIEIVGI	A; Status: preliminary, c A; Molecule type: mRNA A; Residues: 1.420 < GER> A; Cross-references: EMBL	DBJ DN:AAA18498.1;
OY 194 FCSFKIVWSLRRRQOLARQARMK-KATRFIMVVAIVFITCYLP-SVSARLYFLWTVP 248	Query Ma Best Loc Matches	ā.
Qy 249 SSACDPSVHGALHITLSFTYWNSMLDPLVYYFSSPSFPKFYNKLKI 294 ::::	Qy 14 ISQVMPPLLIVAFY ::::	ISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTD 73 ::::
RESULT, 8 A47556 ATP receptor P2u - mouse C;Species: Mus musculus (house mouse) C;Species: Man-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999	:	:
Rilustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D. Rilustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D. Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993 A.Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells. A.Recession: A47556; MUID:93281707 A.Rocession: A47556 A.Status: preliminary A.Molecule type: mRNA A.Molecule type: mRNA	Oy 186 FWPLGILLECSFKI  :          Db 279 FVPFIITTICXIGN   Qy 235 PSVSARLYFLWTVP   Db 338 QEANEFLYFAYIL	FMPLGIILECSFKTWSLRRRQQLARQARMKKATRFIMVVAIVFITGYL 234   :
A;/cross_references: GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458 C;Superfamily: ATP receptor P2u C;Keywords: transmembrane protein	Qy 295 CSLKPKOPGHSKTO     :         Db 382 CCRKVSEPGSSTGO	308 395
Query Match Best Local Similarity 30.1%; Score 320; DB 2; Length 373; Best Local Similarity 30.1%; Pred. No. 5.8e-22; Matches 98; Conservative 44; Mismatches 150; Indels 34; Gaps 8; Qy 4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHWKTWKPSTVYLFNLAVADFL 63	RESULT 10 157940 somatostatin receptor 5 N;Alternate names: somato C;Species: Rattus norveg C;Date: 02-Aug-1996 #seg C;Accession: 157940: 157 R;O'Carroll, A.M.; Lolah Mol. Pharmacol. 42, 939* A;Title: Molecular cloul	RESULT 10 107940 Somatostatin receptor 5. rat N;Alternate names: somatotropin release-inhibiting factor subtype 28 receptor C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Aug-1996 #Seguence_revision 02-Aug-1996 #text_change 24-Nov-1999 C;Date: 02-Aug-1996 #Seguence_revision 02-Aug-1996 #text_change 24-Nov-1999 C;Date: 02-Aug-1996 #Seguence_revision 07-Aug-1996 #text_change 24-Nov-1999 R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C. Mol. Pharmacol. 42, 939-946, 1992 A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with p

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A; Cross-references: GDB:134185; OMIM:182451
A; Map position: 14013-14013
A; Introns: #status absent
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein;
E; 58-44/Domain: transmembrane #status predicted <TM2>
E; 132-12/Domain: transmembrane #status predicted <TM3>
E; 132-15/Domain: transmembrane #status predicted <TM3>
E; 132-15/Domain: transmembrane #status predicted <TM3>
E; 202-250/Domain: transmembrane #status predicted <TM5>
E; 202-250/Domain: transmembrane #status predicted <TM5>
E; 202-250/Domain: transmembrane #status predicted <TM5>
E; 202-250/Domain: transmembrane #status predicted <TM6>
E; 202-250/Domain: transmembrane #status predicted <TM6>
E; 202-250/Domain: transmembrane #status predicted <TM6>
E; 132-250/Domain: transmembrane #status predicted <TM6>
E; 133-250/Domain: transmembrane #status predicted <TM6
E; 133-250
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A;Title: Cloning and functional characterization of a family of human and mouse somat
A;Reference number: A41795; WUID:92108031
    protein-coupled receptor; hormone receptor; transmembrane protein
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 LRYAKMKTATNIYILNLAIADELLMLSVPFLVTSTL-LRHWPFGALLCRLVLSVDAVNMF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCV-Q 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 KRSE-----RKITLMVMMVVMVFVICWMPFYVVQLVNVFAEQDDAT-----VSQLSV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 RRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSACDPSVHGALHITL 264
                                                                                                                                                                                                                                                                                                                                                      24 GACSRGPGSGAADGMEEPGRNASQNGTLSEGQGSAILISFIYSVVCLVGLCGNSMVIYVI 83
                                                                                                                                                                                                                                                                       ----TISOVMPPLLIVAFV-----LGALGNGVALCGF 40
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A;Residues: 1-391 <YAM>
A;Residues: 1-391 <YAM>
A;Cross-references: GB:M81829; NID:g307433; PIDN:AAA58247.1; PID:g307434
A;Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIP:74768)
                                                                                                                                                                                                                                                                                                                                                                                                                                              41 CFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 ETAVSCESFIMESANGWHD---IMFQLEFFMPLGIILFC-----SFKIVWSLR
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                                                                                   Query Match
16.6%; Score 307; DB 2; I
Best Local Similarity 25.7%; Pred. No. 9.9e-21;
Matches 85; Conservative 62; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | :|::| | | :|::| | 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 SFTYMNSMLDPLVYYFSSPSFPKFYNKLKIC 295
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Best Local Simi
Matches 81;
         C; Keywords: G
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R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A;Title Molecular cloning and expression of a pituitary somatostatin receptor with pref A;Reference number: I57949; MuID:94088493
A;Accession: I57949
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Cispecias; Musculus (house mouse)
Cispecias; Musculus (house mouse)
Cispecias; Musculus (house mouse)
Riyamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S. Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A:Title: Cloning and functional characterization of a family of human and mo A:Reference number: A41795; MUID:92108031
A:Reference number: A41795; MUID:92108031
A:Reference number: A41795
A:Refe
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A; Residues: 309-363 <PEN>
A;Cross_references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 CLCYLLIVVKVKAAGMRVGSSRRRRSEPKVTRMVVVVLVFVGCWLPFFIVNIVNLAFTL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 PE---EPTSAGLYFFYVVLSYANSCANPLLYGFLSDNFRQSFRKV-LCLRRGYGMEDADA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 RRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIV 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::| | :: :| || : : | || 39 LVPVLYLLVCTVGLSGNTLVIYVVLRHAKMKTVTNVXILNLAVADVLFMLGLFFLATQNA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 341-363 <CCA2>
A;Residues: GB:S67370; NID:g455947; PIDN:AAB29371.1; PID:g455948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: pituitary
R; Penetta, R.; Greenwood, M.; Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A; Description: Correction of the nucleotide and amino acid sequence of A; Recence number: S39244
A; Accession: S39244
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                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-363 <CCA1>
A; Reference number: 157940; MUID: 93125499
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angiotensin II receptor type 1 - bovine
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C;Accession: S15403
R;Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Mature 351, 230-233, 1991
A;Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angla A;Reference number: S15403
A;Recession: S15403
A;Accession: S15403
A;Accession: S15403
A;Residues: 1-359 <SAS>
A;Residues: 1-359 <SAS>
A;Residues: 1-359 <SAS>
A;Cross-references: GB:X62294; NID:943; PIDN:CAA44182.1; PID:944
C;Superfamily: vertebrate rhodopsin
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A; Residues: 1-369 < YAMY
A; Cross-references: GB:M81830; NID:g307435; PIDN:AAA58248.1; PID:g307436
A; Note: sequence extracted from NCBI backbone (NCBIN:74769, NCBIP:74770)
C; Genetics:
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C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-h
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-h
C; Accession: B41795; Wang, K.; Tager, H.S.; Bell, G.I.; Seino,
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A; Title: Cloning and functional characterization of a family of hums
A; Reference number: A41795; MUID: 92108031
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16.4%; Score 304.5; DB 2;
Best Local Similarity 24.9%; Pred. No. 1.5e-20;
Matches 81; Conservative 68; Mismatches 143;
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A;Map position: 17q24-10
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A; Ross references: GBrafoll4; GB:X61630; NID:956309; PIDN:CAA44193.1; PID:956310
A; Rich X.J.; Forte, M.; North, R. A.; Ross, C.A.; Snyder, S.H.
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A; Title: Cloning and expression of a ret somatostatin receptor enriched in brain.
A; Reference number: A45102; MUID:93016064
A; Recession: A45102
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-391 <LIL)
A; Reperimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP:116692)
C; Superfamily: vertebrate rhodopsin
C; Reywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
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C;Species: Rattus norvegicus (Norway rat)
C;Date: (03-aug-1992 #sequence_revision 03-aug-1992 #text_change 24-Nov-1999
C;Accession: A39297; A45102; S20088
R;Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.
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A;Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expresse
A;Reference number: A39297; MUID:92096119
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C; Superfamily: Vertebrate rhodopsin
C; Superfamily: Vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phd
E; 44-69/Domain: transmembrane #status predicted <TM1>
F; 80-105/Domain: transmembrane #status predicted <TM3>
F; 117-138/Domain: transmembrane #status predicted <TM4>
F; 158-180/Domain: transmembrane #status predicted <TM4>
F; 205-235/Domain: transmembrane #status predicted <TM6>
F; 204-231/Domain: transmembrane #status predicted <TM6>
F; 204-231/Finding site: carbohydrate (Asn) (covalent) #status predicted
F; 115-193/Disulfide bonds: #status predicted
F; 115-193/Disulfide bonds: #status predicted
F; 250/Binding site: phosphate (Ser) (covalent) #status predicted
F; 328/Binding site: palmitate (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 FLVPLTIICLCYLFIIIKVKSSGIRVGSSKRKKSEKKVTRMVSIVVAVFIFCWLP---- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 -FYIFNVSSVSMAISPTPALKGMFDFVVVLTYANSCANPILYAFLSDNFKKSFQNV-LCL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 DYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 AGIVCTLWA---LVILG-TVYLLLENHLCVQETAVSCESFIMESANGWHD----IMFQLE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 LYFLWTVPSSAC----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 TISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFMPLGIILFCSFKIVWSLR----RRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
                                                                                                                                                                                                                                                                                                                                                           16.3%; Score 302.5; DB 2; Length 369; 29.8%; Pred. No. 2.4e-20; Live 50; Mismatches 135; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: October 29, 2002, 04:56:20
Job time : 46 secs
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Best Local Similarity 29.8%
Matches 90; Conservative
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VK 331
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338.050 Million cell updates/sec
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Sequence 4,
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Sequence 3
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1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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US-08-513-974B-374
US-08-513-974B-374
US-08-749-707-4
US-08-179-224A-4
US-08-181-250-2
US-08-181-281-3
US-09-299-843A-44
US-09-299-843A-44
US-09-299-843A-44
US-09-299-843A-44
US-09-427-948A-30
US-08-467-947A-30
US-08-467-947A-30
US-08-467-947A-30
US-08-467-947A-30
US-08-467-947A-30
US-08-467-947A-30
US-08-467-947A-30
US-08-467-947A-30
US-08-118-270-51
PCT-US93-0828-51
US-08-118-270-51
US-08-417-103-4
US-08-417-103-4
US-08-417-103-4
US-08-917-00-5
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                              October 29, 2002, 04:47:16
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match
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                                                                                                                                                                                                                                                                                                                                    Perfect score:
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                                                                                           Sequence 6, Assequence 6, Assequence 6, Assequence 6, Assequence 9, Assequence 2, Assequence 2, Assequence 6, Assequence 16, Assequence 2, Ass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1.2 Application US/08955713

Patent No. 595308

GENERAL INFORMATION:
APPLICANT: SATHE;
APPLICANT: BERGSMA, DERK
APPLICANT: HALEST, WENDY
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
COUNTRY: USA
ZIP: 19482
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US-08-476-976-5
US-08-474-410-5
US-08-097-98-6
US-08-476-000-6
US-08-476-976-6
US-08-474-410-6
US-08-474-410-6
US-08-417-410-6
US-08-417-103-1
US-08-120-601B-9
US-08-120-601B-9
US-08-120-601B-9
US-08-120-601B-8
US-08-120-601B-8
US-08-120-601B-8
US-08-120-601B-8
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US-08-120-601B-8
US-08-120-601B-8
US-08-120-601B-8
US-08-120-601B-8
US-08-117-103-16
US-08-117-103-16
US-08-117-103-16
US-08-417-103-16
US-08-418-13-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 423 amino acid
TYPE: amino acid
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Best Local Similarity 39.2%
Matches 115; Conservative
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MEDIUM TYPE: Diskette
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      STRANDEDNESS:
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US-08-955-713-2
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US-08-955-713-2
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138 TEWALVILGTVYLLLENHLCVQETAVSCESFIM----ESANGWHDIMFQLEFFMPLGIIL 193
                                                                                                                                                                                                                                   FCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV---SARLYFLWTVPSS 250
                                                                            78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                        6 LAPILALEFYLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFLLISNLPLRVDYYLL 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHABON, USMAN
ELSHOURBAGY, NABIL
TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
RECEPTOR (GPR31A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                               251 A---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                   SEDICTQLFHG---SLAFTYLNSVLDPVLYCFSSPNF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 451.5; DB
; Pred. No. 1.1e-31
61; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,749
FILING DATE: 07-Aug-1998
CLASSIFICATION UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: CURNOWN>
FILING DATE: CURNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: PRESTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: Innear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-130-749-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSE: RAYNER & PRESTIA
STREET: P.O. BOX 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09130749 Patent No. 6031090 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 319 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEFAX: 610-407-0701
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 34.4%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                        LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                                                                      124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
                                                                                                                                                                                                179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
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                  GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL
                                                                                                                                                                                                                                                                                                                                 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
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39.6%; Pred. No. 1.6e-36;
Live 47; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GERERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: MOONEY, JEFFREY
APPLICANT: HALSEY, WENDY
ITILE OF INVENTION: CDNA CLONE HEOAD54 THAT ENCODES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: RATHORR & PRESTIA
STREET: PO. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,713
FILING DATE: 23-0CT-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 60/050,124
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
ANDER APPLICATION NUMBER: MANUEL PROGRATION:
ANDER APPLICATION NUMBER: MANUEL PROGRATION:
ANDER APPLICATION NUMBER: MANUEL PROGRATION:
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REGISTRATION NUMBER: 23,031
REFERENCE/ZOCKET NUMBER: GH-70087
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08955713
Patent No. 5955308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476 amino acids
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: sin
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Matches 110; Conserv
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US-08-955-713-4
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126 LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182
                    67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                               127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF
                                                                                                                                                                            183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR
                                                                                                                                                                                                                                                                           243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVYYCFSSPTFRSSYRRV 296
                                                                                                                                                                                                                                                        241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
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APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
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FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 374, Application US/08513974B Patent No. 6114139 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
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CITY: Boston
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Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fukusumi, Shoj:
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APPLICANT: Ohg1, Kazuhiro
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Fujii, Ryo
Ohtaki, Tets
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APPLICATION NUMBER:
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TITLE OF INVENTION: PRA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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                                                                                182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                                                                                                                                                                                                                                    127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
                                                        67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
6 CSAPSTVVATAVGVLLGLECGLGLIGNAVALWTFFRVRVWKPYAVYLLNLALADLLLAAA 65
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Patent No. 6031344
GENERAL INPORMATION:
APPLICANT: SHABON, USMAN
TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
TITLE OF INVENTION: RECEPTOR (GPR31A)
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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; Pred. No. 1.1e-31;
61; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,749
FILING DATE: 07-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: RATNER & PRESTIA
STREET: P.O. Box 980
CITY: Valley Forge
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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; MOLECULE TYPE: protein
US-09-130-749-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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COUNTRY:
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Best Local 9
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78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRLSR----- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP----SVSAR
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Patent No. 6063582

GENERAL INFORMATION:
APPLICANT: COLOLey, Pamela B.
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
STREET: D.C.
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,707
    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                            19.6%; Score 362.5; DB 2; 27.5%; Pred. No. 6.5e-24; Live 68; Mismatches 140;
                                                                                                                                                                   044481-5010-00-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 --ATRKASRRSEANLOSKSEDMTLNILSEFKONGD 370
                                                                             CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 04441
TELEPHONE: 202-467-7000
TELEPHONE: 202-467-7176
                                                        15-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  LENGTH: 373 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                       TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                         APPLICATION NUMBER:
FILING DATE: 15-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20036-5869
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Matches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-749-707-4
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MKTLNLRARLDF-QTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLWALVILGTVYLLLENHL------CVQETA-----VSCESFIMESANGWHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP--- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||||:
| S TVWALVVAVIAPILEYSGIGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.0%; Score 371; DB 3; Length 36
29.1%; Pred. No. 1.2e-24;
tive 60; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08559524A
Patent No. 5871963
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: MORGAN, LEWIS & BOCKIUS LLP
1800 M Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 LKICSLKPKQPGHSKTQRPEEMPISNL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 ATRKSSRRSEP--NVQSKSEEMTLNIL 351
                                                      APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
    JP 6-189274
                                                                                                                                                                                                                              45753
                                                                                                                                                                                NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFRENCE/DOCKET NUMBER: 4575:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS:
APPLICATION NUMBER: JP 6-
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 29.12
Best Local Similarity 29.12
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
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Gaps

Length 373;

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48 VVFILGLITUSVSLFVFCFRRMKMRSETAIFITNLAVSDLLFVCTLPFKI-FYNFNRHWPF 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 CSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSAC- 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 ----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKLKICSLKPKQPGHSK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 VILGTVYLLLENHLCVQETAVSC-ESFIMESANGWHDIMFQLE-----FFMPLGIILF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 44, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vacki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago CITY: 1111nois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.7%; Score 346.5; DB 3; 31.2%; Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52; Mismatches 128;
                                                                                       ATTORNEY AGENT INFORMATION:
NAME: William T. Han,
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50043
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4060
                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bicknell
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 TQRP 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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APPLICANT: Sathe, Ganesh
APPLICANT: Sathe, Ganesh
APPLICANT: Sathe, Ganesh
APPLICANT: Sathe, Ganesh
APPLICANT: Bergsma, Derk
APPLICANT: Mao, Joyce Yue
TITLE OF INVENTION: CDNA CLONE HE8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham
STRRET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----SVSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR-----
                                                                                                                                                                                                                                                                                                                                                                                                   Length 373;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
19.6%; Score 362.5; DB 3; Length 3
Best Local Similarity 27.5%; Pred. No. 6.5e-24;
Matches 92; Conservative 68; Mismatches 140; Indels
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
TTORNEY/AGENT INFORMATION:
NAME: AAGENT REIGHT 810,988
RECISTRATION NUMBER: 30,988
RECISTRATION NUMBER: 30,988
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-467-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,250
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- ATRKASRRSEANLOSKSEDMTLNILSEFKONGD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08781250 Patent No. 6010877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPALIDLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-707-4
                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
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Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Borun
ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.5%; Pred. No. 1.1e-21;
Matches 97; Conservative 54; Mismatches 153; Indels
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OPERATING SYSTEM: DOS
SOFTWARE: FRASLESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAMME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0237 US
TELEPHONE: 415-85-055
TELEPHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 PKQPGHSKTQRPEEMPIS 316
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                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 18.1%; Score 336; DB 1; Length 33: Best Local Similarity 30.5%; Pred. No. 1.1e-21; Matches 97; Conservative 54; Mismatches 153; Indels
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APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Incyte Pharmaceuticals, Inc.
3174 Porter Dr.
                                    FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759604and, Greta E.
REGISTRATION NUMBER: 35,302
RECENENCE/DCCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08812871 Patent No. 5955303 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 PKQPGHSKTQRPEEMPIS 316
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                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-153-848-44
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CITY: Palo Alto
STATE: CA
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84 EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
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                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                      STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
18.1%; Score 336; DB 4; L
Best Local Similarity 30.5%; Pred. No. 1.1e-21;
Matches 97; Conservative 54; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
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PCT-0593-11153-44
Sequence 44, Application PC/TUS9311153
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                     COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM: MEDIUM TYPE: FLORPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312) 474-0448
TELEX: 25-386
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 339 amino acids
NUMBER OF SEQUENCES: 66
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                        CORRESPONDENCE ADDRESS
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                                                                                                              CITY: Chicago
STATE: Illinois
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Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Mismatches 153; Indels
                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: J111 E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKEY NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UN-1998
PRIOR APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/157,452
FILING DATE: 17-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          APPLICATION NUMBER: US/09/299,843A
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity
                                                                                                                                                                                  FILING DATE:
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Indels

Length 339;

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GENERAL INFORMATION:
APPLICANT: LI, YI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 CGQETPLENMLFASFYLLDFILALVGNTLALMLFIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.1%; Score 336; DB 5; Length 339; 30.5%; Pred. No. 1.1e-21; tive 54; Mismatches 153; Indels
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwalkart, Vicki L.
TITLE OT INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                               6300 Sears Tower, 233 South Wacker Drive
                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/1115
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application PC/TUS9507180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (312) 474-6300
TELERX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Noland, Greta E. REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 31. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 PKQPGHSKTQRPEEMPIS 316
                                                                                                                                                                                                                                                                 Floppy disk
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amino acid
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Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-44
                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                        Illinois
                                                                                                                                                   STREET: 6300 8
CITY: Chicago
                                                                                                                                                                                                           USA
                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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PCT-US95-07180-2
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127 ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.1%; Score 336; DB 5; Length 339
30.5%; Pred. No. 1.1e-21;
Live 54; Mismatches 153; Indels
                                                                                                                                               ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD STREET: ROSELAND STATE: NOSELAND
                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICANT: LI, YI
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUTAING APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-467-948A-30
S-08-467-948A-30
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 32.80, 073
REFRENCE/DOCKET NUMBER: 32.80
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1704
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 PKQPGHSKTQRPEEMPIS 316
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amino acid
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Best Local Similarity 30.5%
Matches 97; Conservative
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MOLECULE TYPE: protein

PCT-US95-07180-2
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ZIP: 07068
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                              APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: GENTZ, REINER
APPLICANT: GUTZ, CAROL J.
APPLICANT: BULT, CAROL J.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESSONDEMCES: STERNE, RESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 302;
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: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: MASHINGTON COURTY: NW, SOILE DOUGLEY: MASHINGTON STATE: DC COUNTRY: USA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK COMPUTER: PELPOSY MS-DOS SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,948A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION 433
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFRENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 30.2 amino acids TYPE: amino acid sTRANDEDNESS: single TOPOLOGY: not relevant MOLECULE TYPE: peptide
CAO, LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-467-948A-30
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Perfect score:

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Scoring table:

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AJ300199 Mus muscu
AR030624 Sequence
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AX148166 Sequence
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Y12366 H.sapiens m
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AL121935 Human DNA
AL353591 Homo sapi
AX224752 Sequence
AX334111 Sequence
AX335616 Sequence
U65402 Human seven
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AC098824 Homo sap1
AR075072 Sequence
E31721 cDNA clone
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AX26533 Homo Sap1
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Jases 1 to 1041)

Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,

Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,

Sejlitz,T. and Huff,R.M.

Novel g protein-coupled receptors

Patent: WO 0136473-A 79 25-MAY-2001;

PHARMACIA & UPJOHN COMPANY (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                        TTCATCATGGTGGTGCCAATTGTGTTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
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 GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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adjunder, V. Vernet, C.A., Casman, S.J., Wolenc, A.R., Spadern
Padjuaru, M., Mishnu, V.S., Tchernev, V.T., Spytek, K.A., Li, L.
Baumgartner, J.C. and Gusev, V.Y.
Bovel proteins and nucleic acids encoding same
Patent: WO 01/1904-A 1 11-OCT-2001;
Curagen Corporation (US)
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100.0%; Pred. No. 3.5e-249;
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/product="G protein_id="AAL26481.1"
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KTWKPSTVYLFNLAVADFLIMICLPFRIDYILRRHWAFGDIPCRVGLFTLAMNRAGS
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TAVSCESFIRESANAHDINFOLEFFWPLGITLFGFKTWASLEFRROGLARGARKKA
TRFIMVVAIVFTTCYLDSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPL
VYTESSPFERFYNKLKICSLKPKOPGGHSKTQRPEEMPISNLGRRSCISVANSFQSG
Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
Discovery and mapping of ten novel G protein-coupled receptor genes 215 (1), 83-91 (2001)
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                                                                                                           Lee, D. K., Nguyen, T., Lynch, K. R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.

Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.

Submitted (17-AUG-2001) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, ont M5S 1A8, Canada Location/Cualifiers

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/organism.Homo sapiens*
/db.xref="taxon:9606"
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Majunder,K., Vernet,C.A., Casman,S.J., Wolenc,A.R., Sp
Padigaru,M., Mishnu,V.S., Tchernev,V.T., Spytek,K.A.,
Baumgartner,J.C. and Gusev,V.Y.
Novel proteins and nucleic acids encoding same
Patent: WO 0174904-A 3 11-OCT-2001;
Curagen Corporation (US)
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Sequence 3 from Patent WO0174904
AX338373
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Oy 661 TTCATCATGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA 720 	Qy 721 CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGCCCTG 780	781 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGGTCCCCTGGTGTTTTTTTT	841 TCAAGCCCTCCTTTCCCAAATTCTACAAGCTCAAAATTCTGAAACTCGAAGTCTGAAACCCAAG 90	901 CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGGCCAATTTCGAACCTCGGTCGC	961 AGGAGTTGCATCAGTATACACAGTATCCAAAGTACCAAATITCGATCCTCGGTCCC 961 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC	1021 CACATTGTTGAGTGGCACTGA 1041 1021 CACATTGTTGAGTGGCACTGA 1041 1036 CACATTGTTGAGTGGCACTGA 1046	FOT 40 120 120 120 120 120 120 120 120 120 12	AX305131 N Sequence 11 from Paten AX305131	99	ŭ · 、		JOURNAL Patent: WO 0187937-A 11 22-NOV-2001; Incyte Genomics, Inc. (US) FEATURES Location/Qualifiers Source 11083	/organism="Homo sapiens" /db_xref="taxon:9606" /note="Incyte ID No: 7474846CB1" 211 a 314 c 288 g 270 t	Query Match 100.0%; Score 1041; DB 6; Length 1083; Best Local Similarity 100.0%; Pred. No. 3.5e-249; Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy     1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGACACCATCTCCCAGGTGATGCCGCCG     60       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy     61     CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCGTCGCCCTGTGTGGTTTC     120       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTACCTTTTCAATTTGGCCGTGGCT 180 

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PE Corporation (NY) (US)
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/db_xref="taxon:9606"
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Sequence 3 from Patent W00173029,
AX299707 GI:17129251
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 Regulation of human hm74-like g protein coupled receptor Patent: WO 01773-0.A 1 la CocT-2001; Bayer Aktiengesellschaft (DE) Location/Qualifiers
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/db_xref="taxon:9606"
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	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL		
ACGCCGTCTCCTGTGAGGGCTTCATCATGGAGTCGGCCAATGGCTGGC	CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTT  [	AGGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTGTGGGCAATGGGATCCC 1020 [	ACO26331  Homo sapiens chromosome 12 clone RP11-507N20, WORKING DRAFT SEQUENCE, 10 unordered pieces.  NACO26331.8  ACO26331.18  ACO26331.18  GI:1454738  HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.  Homo sapiens  EUKARYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens  EUKARYOCA; Malone Control Contr
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S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Li, J., Li, E., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Eddo, R.J., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Edd, M., Mapue, P., Martin, R., Martindale, A.,
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E., Massey, E., Mawhiney, E., Micched, M. E., Meador, M.,
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Nerz, L., Peters, L., Pickens, R., Pilmus, E., Pu, L. L.,
Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
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Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N.,
Wang, S., Wald-Moore, S., Warren, R., Washington, C.,
Wang, S., Wallams, G., Williamson, A., Wleczyk, R., Wooden, S.,
Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
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Well, M., Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Well, M., Y., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Well, M., Y., Wu, Y., Wu, Y., Wu, C., Wu, C., Wu, Y., Wu, Y., Wu, C., Wu, Y., Wu, C., Wu, Y., Wu, C., Wu, Y., Wu, Y., Wu, C., Wu, Y., Wu
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----- Summary Statistics
encing vector: Plasmid: M7789
encing vector: H13: L08621
encing vector: M13: L08621
encing program: Phrap: version 0.990329
ensus quality: 178511 bases at least Q30
ensus quality: 179678 bases; at least Q30
ensus q40418 bases; at least Q30

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s is a 'working draft' sequence. It currently of 10 contigs. The true order of the pieces own and their order in this sequence record is Gaps between the contigs are represented as , but the exact sizes of the gaps are unknown. It will be updated with the finished sequence it is available and the accession number will ved.
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Baylor College of Medicine
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i hgsc.help@bcm.tmc.edu
--- Project Information
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1352 167351: contig of 6274 bp in length 1352 167451: gap of unknown length 1452 173489: contig of 5938 bp in length 1390 173489: gap of unknown length 1490 176258: contig of 2769 bp in length 1558: gap of unknown length 1359 176358: gap of unknown length 1359 179172: contig of 2814 bp in length 16cation/Quallifiers
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100.0%; Pred. No. 5e-249;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-507N20"
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09 910 TCAAGCCCTCCTTTCCCAANTTCTACAACACCTCCAATTCACCTCGTCGTCGAATTATTT 12185

09 910 TCAAGCCCTCCTTTCCCAANTTCTACAACACCTCCAATTCTCCAATTCTCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCCAATTCTCAATTCTCCAATTCTCAATTCTCCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTC
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                                                                                                                                                                                                                                   Sequencing vector: Plasmid: M77789
Sequencing vector: Plasmid: M77789
Sequencing vector: M3: L08821
Chemistry: Dye-primer Bodipy: 8% of reads
Chemistry: Dye-primer Bodipy: 8% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 208562 bases at least Q40
Consensus quality: 208562 bases at least Q30
Consensus quality: 210152 bases at least Q30
Estimated insert size: 205209; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                        Submitted (22-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 30, 2001 this sequence version replaced g1:14861654.
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gap of unknown length
contig of 18253 bp in length
gap of unknown length
contig of 11275 bp in length
gap of unknown length
contig of 11301 bp in length
gap of unknown length
gap of unknown length
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gap of unknown length
contig of 43017 bp in length
gap of unknown length
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                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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Center clone name: RP11-324E6
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               2 (bases 1 to 204062)
Worley, K.C.
Direct Submission
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100.0%; Score 1041; DB 2; 100.0%; Pred. No. 5.1e-249;
                                       Mismatches
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1021 CACATTGTTGAGTGGCACTGA 1041

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PAT 08-JUN-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 888)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Silghtom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejligt,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 11 25-MAY-2001;
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Best Local Similarity 100.0%; Pred. No. 5.3e-211;
Matches 888; Conservative 0; Mismatches 0;
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Sequence 11 from Patent WO0136473.
AX147766
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Majumder,K., Vernet,C.A., Casman,S.J., Wolenc,A.R., Spaderna,S.K., Padigaru,M., Mishnu,V.S., Treernev,V.T., Spytek,K.A., Li,L.,
Baumgartner,J.C. and Guesev,V.Y.
Novel proteins and nucleic acids encoding same
Patent: WO 0174904-A 4 11-OCT-2001;
Curagen Corporation (US)
                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.2e-
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/organism="Homo saplens"
/db_xref="taxon:9606"
318 c 295 g 275
                                                                     Sequence 4 from Patent WO0174904.
AX338374
Db 16591 CACATTGTTGAGTGGCACTGA 16611
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Best Local Similarity 99.8
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atch 35.5%; Score 369.2; DB 6; Length 1092; cal Similarity 64.0%; Pred. No. 1.7e-81;	VALLYE V, MISMACCHES CGTGCTGCCGCATCGAGGGGGACACC                     ACTGCTGTGTGTTCCGAGATGACTTC	Qy 61 CTGCTCATTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120	Qy 121 IGCTICCACATGAAGACCTGGAAGCCCAGCACTGTTTACATTTGGCCGTGGCT 180	Qy 181 GATTICCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240	Qy 241 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC 300	Qy 301 GGGAGCATCGTGTTCCTTACGGTGCTGCGGGCAGGTATTTCAAAGTGGTCCACCCC 360	Qy         361 CACCACGCGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCTGTGG         420	Qy 421 GCCCTGGTCATCCTGGGAACAGTGTATCTTTGCTGGAGAACCATCTGTGCGTGC	OY 481 ACGGCCGTCTCCTGTGAGAGCTTCATCATGGAGTCGGCCAATGCTGGCATGACATG 540	Qy 541 TTCCAGCTGGAGTTCTTTATGCCCTCGGCATCATTTTGCTCCTTCAAGATTGTT 600	Oy 601 TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG 660	Qy   661 TTCATCATGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA 720	766 GTCGATGGGGCCCTGCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCC   11   1   1   1   1   1   1   1   1		Qy 886 AGTCTGAAACCCAGGACAGTCAAAAA 919 	RESULT 15 AX335595 2051 bp DNA linear PAT 09-JAN-20
241 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC 300	GGGAGCATCGTGTTCCTTACGGTGGTGGTCGCCGACACGTTTCAAAGTGGTCCACCCCCCCTTACAAGTGGTCCACCCCCCCC	361 CACCACGCGGTGAACACTATCTCCACCCGGTGGCGGCTGGCATCGTCTGCACCCTGTGG 420 	421 GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAACCATCTCTGCGTGCAAGAG 480 	481 ACGCCCGTCTCTGTGAGAGCTTCATCATGGAGTCGCCAATGGCTGGC	541 TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT 600	601 TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG 660 	661 TTCATCATGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGGGTGTCTGCTAGA 720 	721 CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG 780 (IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	781 CACATAACCTCAGGTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTT 840 	841 TCAAGCCCTCCTTTCCCAATTCTACAAGACTCAAAATCTGCAGTCTGAAACCCAAG 900 	901 CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGATGCCCAATTTCG 948 	RESULT 14 AX148194 AX148194 AX148194 AX148194 DEFINITION Sequence 35 from Patent W00136471. ACCESSION AX148194 AX148194 AX148194 AX148194	S human. ISM Homo sapiens Elekaryota; Metazoa; Chordata;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1092) Chen, R., Dang, H.T. and Lowitz, K.P. Endogenous and non-endogenous versions of human g pro	receptors JOURNAL PAtent: WO 0136471-A 35 25-MAY-2001; Arena Pharmaceuticals, Inc. (US) ATURES Location/Qualifiers	T 223 a
Š d	oy da	oy Op	Oy Db	Oy Dp	oy Dp	Oy Db	Oy Db	Qy Db	Qy Dp	Qy Db	Oy Dp	RESULT 14 AX148194 LOCUS DEFINITIO ACCESSION	KEYWORDS SOURCE ORGANI	REFERENCE AUTHORS TITLE	JOURNA FEATURES	BASE

09-JAN-2002

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1 (sites)
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D. R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
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                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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Pred. No. 4.5e
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Sequence 6104 from Patent W00194629
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GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	cDNA encoding nove	Human cDNA encodin	Human nGPCR11 cod1	Human GPCRla polyn	Human GPCR1b polyn	Human G-protein co	cDNA encoding HM74	Gene encoding nove	Human GPCR1c polyn
LES				:								
SUMMARIES			Ω	AAS12581	AAS07946	AAH51008	ABA81529	ABA81530	AAD26371	AAS18501	AAS12582	ABA81531
			8	22	22	22	22	22	24	24	22	22
			Match Length DB	1041	1041	1041	1050	1050	1083	1730	2331	1104
	ф	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.2
			Score	1041	1041	1041	1041	1041	1041	1041	1041	626
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Human nGPCR11 codi Human G protein-co DNA encoding human G-protein coupled Oligonucleotide SE Human nGPCR11 PCR Oligonucleotide SE Human nGPCR11 PCR Oligonucleotide SE Human nGPCR11 PCR	Human nuccril pCR Human musculoskele Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog DNA encoding novel Human low density Drosophila melanog Nucleotide sequenc Secreted protein C Secreted protein C Human polynucleoti EST clone C195. H Human polynucleoti Human cardiovascul Human cardiovascul Human cardiovascul Human cardiovascul Secreted protein C Human neuroblastom N. meningitidis pa	pled receptor (GPCR).  ; chemokine receptor; protease;  id disorder; psychabric disease;  rder; gene therapy; ss.
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The present invention relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor subfamily. The CDNA and gene sequences encoding for GPCR are also given in the invention. The sequences of the invention are useful for diagnosing and treating diseases or conditions mediated by human for diagnosing and treating diseases or conditions mediated by human cereptor diseases. Such diseases include hyperpoliferative disorders (e.g. hyperplasia), neurological disorders (e.g. parkinson's disease), psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g. adult respiratory distress syndrome, ARDS). The GPCR protein is also useful for identifying distress syndrome, ARDS). The GPCR protein is also serves as a target for identifying agents for use in mammalian therapeutic applications, cerify a human drug, particularly modulating a biological or pathological response in a cell or tissue that expresses the protein, in biological ceptor subfamily, in drug screening assays and in competition binding assays. GPCR is also useful in diagnosing a disease or predisposition to a disease mediated by the peptide, in pharmacognomic analysis. The copynucleotide sequences can also be used in gene therapy. The present sequence encodes for the novel human GPCR of the invention.
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                                                                                                      Novel human G-protein coupled receptor proteins and nucleic acid molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the
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                                                                                                                                                                                                           coupled receptor; GPCR; hRUP19; agonist; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA encoding G-protein coupled receptor, hRUP19.
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99US-0166369.
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11-FEB-2000;
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G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autolmmune disorder; respiratory ailment;
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                                                                                                                                                                                                                                                                                                                                                                Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
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100.0%; Score 1041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1041; Conservative 0; Mismatches
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14-MAR-2000; 2000US-0189258.
14-MAR-2000; 2000US-0189259.
10-APR-2000; 2000US-0195898.
10-APR-2000; 2000US-0195899.
10-APR-2000; 2000US-0196078.
28-APR-2000; 2000US-0200419.
12-JUN-2000; 2000US-021041.
12-JUN-2000; 2000US-0210982.
21-AUG-2000; 2000US-0210982.
21-AUG-2000; 2000US-0215418.
26-SEP-2000; 2000US-0235418.
26-SEP-2000; 2000US-0235779.
26-CGT-2000; 2000US-0235779.
                                                                                                                                                                                                                                                                                     Dang HT, Lowitz KP;
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Best Local Similarity
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Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimær's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
                                                                                          GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present c sequence is the coding sequence for one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for c screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of c nGPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular disorders, infections deform and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, cincluding schizophrenia, ADHD/ADD (attention deficit disorder), and neuronal disorders such as Alzheimer's disease, prothics and certains of disorders such as Alzheimer's disease, prothics and certains and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's concers), recommenders, cancers, cancers, respiratory allments such as asthma, and inflammatory diseases e.g.
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PS, Bannigan CM, Ruff V, Sejlitz T, Huff
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 89; 261pp; English.
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                                                                                                        2000US-0186530.
2000US-0186811.
2000US-0188114.
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2000US-0198568.
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99US-0165838.
99US-0166071.
99US-0166678.
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2000US-0207094.
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2000US-0185554
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Best Local Similarity 100.(
Matches 1041; Conservative
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Schellin KA, Kaytes
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28-FEB-2000;
02-MAR-2000;
03-MAR-2000;
09-MAR-2000;
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21-MAR-2000;
20-APR-2000;
02-MAY-2000;
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25-MAY-2000;
                                                              22-FEB-2000;
                                             28-DEC-1999;
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                        05-APR-2000;
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06-APR-2000;
11-JUL-2000;
  Homo sapiens
                                              27-JUL-2000;
28-JUL-2000;
                                                                   29-MAR-2001;
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SK; Spaderna S L1 L; Wolenc AR, Spytek KA, Vernet CAM, Casman SJ, Mishnu VS, Tchernev VT, 28-JUL-2000; 2000US-221325P. 11-AGC2000; 2000US-22458BP. 11-CCT-2000; 2000US-22458BP. 18-JAN-2001; 2001US-26250BP. 23-JAN-2001; 2001US-26433P. 23-JAN-2001; 2001US-26644P. 2000US-195068P. 2000US-195069P. 2000US-195070P. 2000US-195510P. 2000US-219855P. 2000US-221284P. 30-MAR-2001; 2001WO-US10241 2000US-195066P 2000US-195067P 2001US-0823172 Gusev VY; CURA-) CURAGEN CORP.

New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and agonists useful therapeutically agonists useful therapeutically

Claim 9; Page 7; 157pp; English.

The invention relates to nucleic acid sequences (ABAB1529-ABAB1552) that encode G-coupled protein-receptor related polypeptides

C (ABB4522-ABB4643). The isolated polypeptides

C (CPCRX) polypeptides. The polypeptides have potential cardiant.

C (CPCRX) polypeptides. The polypeptides have potential activity. The properties can be administered therapeutically, especially using gene therapy and expressing the encoding DNA in vivo, to treat or prevent cardiomyopathy, atherosclerosis, disorders can be used to treat/prevent cardiomyopathy, atherosclerosis, disorders can be used to also and metabolic pathway modulation (e.g. cobssity, anorexia), diabeters, osteoporosis, Crohn's disease, multiple cobssity, anorexia, disorders, neurodegenerative disorders, davaders, osteoporosis, Crohn's disease, multiple cobssity, anotozoal and viral infections (e.g. with human communication) protozoal and viral infections (e.g. with human communication in polypeptide expression levels relative to determine the presence of or predisposition to a disease associated with altered levels of the polypeptide expression levels relative to determine the presence of or predisposition to a disease associated with altered levels of the polypeptide expression levels relative to determine the presence of or predisposition to a disease associated with altered levels of the polypeptide expression levels relative to determine the presence of or predisposition to a disease associated with altered levels of the polypeptide expression and/or agents

C control samples. They are useful to identify agents binding polypeptide apparent to a disease assoc antagonists and agonists in disease treatment.

Sequence 1050 BP; 211 A; 299 C; 279 G; 261 T; 0 other;

305 365 420 425 480 485 540 545 605 9 720 725 840 845 61 CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGTTTC 120 Gaps 9 65 186 GATTICCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 246 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC 66 CIGCICATIGIGGCCITIGIGCIGGCGCACIAGGCAAIGGGGTCGCCCIGIGIGITIC TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG CTCTATTTCCTCTGGACGGTGCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC GGGAGCATCGTGTTCCTTACGGTGGTGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGAGCCCGG TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG ö Indels ó Score 1041; I 0; Mismatches 100.0%; 100.0%; Conservative Similarity Best Local Sim Matches 1041; 9 301 306 361 366 486 909 999 984 901 196 996 121 421 126 481 541 546 601 199 721 726 781 841 846 ð 염 à g ð g ò g ò g ò d ò g à a δ a ò g ò g ð a ò a ò g ò g ò g à g

especially using gene

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polypeptides can be administered therapeutically,
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                                                                                                                                                                                                                                                                                                           antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                       anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzhelmer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
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Spytek KA,
                                                                                                                                                                                                                                                                                                         GCPR; G-coupled protein-receptor;
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Padigaru M, Mishnu VS, Tchernev VT,
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    1021 CACATTGTTGAGTGGCACTGA 1041
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P-PSDB; ABB44522.
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therapy and expressing the encoding DNA in vivo, to treat or prevent CC CPCRX-associated disorders, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atheroscierosis, disorders related to signal processing and metabolic pathway modulation (e.g. related to signal processing and metabolic pathway modulation (e.g. obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's disease, parkinson's disorders, immune disorders, bacterial, fungal, protozoal and viral infections (e.g. with human immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically to detecting alterations in polypeptide in mammals (especially humans) by detecting alterations in polypeptide in mammals (especially humans) by detecting alterations in polypeptide expression levels relative to control samples. They are useful to identify agents binding polypeptide expression or activity, useful as metagonists and agonists in disease treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1050 BP; 211 A; 298 C; 279 G; 262 T; 0 other;
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                                                                                                                                                                                                                                                                                                                        arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy; Alzhahmer's disease; parkinson's disease; cardiovascular disorder; atherosclerosis; hypertension; myocardial infarction; peptic ulcer; gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder; acquired immune deficiency syndrome; inflammatory disorder; infection; Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS; diabetes; obesity; osteoporosis; gene therapy; GCREC-3; ss.
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                                                                    841 TCAAGCCCCTCCTTTCCCAAATTCTACAAGCTCAAAATCTGCAGTCTGAAACCCAAG
                                                                            CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC
                                           CICTAITICCICTGGACGGIGCCCTCGAGIGCCTGCGATCCCTCTGTCCATGGGGCCCTG
                                                                                                                  Hafalia A;
Au-Young J;
                                 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
                                                                                                                                                                                                                                                                                                                Human; G-protein coupled receptor 3; cell proliferative disorder.
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/product= "Human mature GCREC-3 protein"
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/product= "Human GCREC-3 protein"
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Elliott VS,
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25-MAY-2000;
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The invention relates to numan G-protein coupled receptor (GCKEC)

To polypeptides and polynucleotides. GCREC polypeptides are useful for screening compounds that modulate their activity. They are useful in the dagnosis, prevention and treatment of disorders which include cell proliferative disorders such as arteriosclerosis, hepatitis, myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia, lymphoma; neurological disorders such as epilepsy, isochemic creebrovascular disease, Alzheimer's disease, Fick's disease, dementia, parkinson's disease, ataxias, multiple sclerosis, bacterial and viral mentiquits, Creutzfeldt-Jakob disease, schizophenic disorders, ammesia; cardiovascular disorders such as arteriovenous fistula, atherosclerosis, hypertension, vascular tumours, myocardial infarction, hypertensive cardiovascular disorders such as dysphagia, peptic osophagitis, gastrointestinal disorders such as dysphagia, peptic osophagitis, emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea, constipation, acquired immune deficiency syndrome (AIDS), hepptic encephalopathy; autoimmune/Ainflammatory disorders such as Addison's disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, emphysema, Grave's disease, diabetes mellitus, Goodpasture's syndrome, emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, uveitis, viral, bacterial, fungal, parasitic, protozoal and helminthic infections and trauma; metabolic disorders such as diabetes, obesity and osteoporosis; and cadenovirus, annavirus, bunyavirus. Polynucleotides of the invention are useful as probes for assessing toxicity of test compounds. They are also used in gene therapy. The peptic sequence is human G-protein
                                                                                                                        Novel G-protein coupled receptors and polynucleotides useful for diagnosis, treatment and prevention of disorders of cell proliferation, neurological, cardiovascular, metabolic disorders and viral infections
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                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human G-protein coupled receptor (GCREC)
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100.0%; Score 1041; DB 24; Length 1083;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1041; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 112; 115pp; English.
WPI; 2002-089844/12.
P-PSDB; AAE16172.
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/note= "G-protein coupled receptor"

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AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
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                                                                                                                                                                           TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG
                                                                                                                                                                                                  CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGAGATGCCAATTTCGAACCTCGGTCGC
                                                                 TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTTGCTCCTTCAAGATTGTT
                                                                                                                                                   CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT
                                                                            TGGAGCCTGAGGCGGAGCAGCAGCTGGCCAGCCAGGCTCGGATGAAGAAGGCGACCCGG
                                                                                                   TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
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                                                                                                                                                       protozoacide; analgesic; cytostatic; neuroleptic; nootropic; analgesic; cytostatic; neuroleptic; nootropic; bulimia; asthma; central nervous system disease; CNS disease; cardiovascular disease; hypotrension; hypertension; angina pectoris; myocardial infarction; urinary retention; osteoporosis; ulcer; asthma; inflammation; allergy; benign prostatic hypertrophy; multiple sclerosis; psychotic disorder; neurological disorder; dyskinesia; huntington's disease; Tourette's syndrome; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; ss.
                                                                                                                             HM74-like GPCR; G-protein coupled receptor; antibacterial; fungicide;
                                                              cDNA encoding HM74-like G-protein coupled receptor (GPCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
464..1504
26-FEB-2002 (first entry)
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/product- "HM74-like\_GPCR"

Homo saptens

AAS18501;

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The invention describes a novel isolated polynucleotide (I) encoding a human HM74-like GPCR are useful for modulating the activity of that regulate HM74-like GPCR are useful for modulating the activity of the regulate HM74-like GPCR are useful for modulating the activity of the protein in a disease selected from bacterial, fungal, protozoan, and viral infection, pain, cancer, anorexia, bulimia, asthma, central nervous system (CNS) disease, cardiovascular disease, hypotension, hypertension, angina pectoris, myocardial infarction, urinary retention, osteoporosis, ulcar, asthma, inflammation, allergy, benign prostatic hypertrophy, culer, asthma, inflammation, allergy, benign prostatic hypertrophy, culer, syndrome. The composition is also useful for treating psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, delirium, dementia and severe mental retardation. (I) cor the HM74-like GPCR polypeptide are also useful for treating the above cor the HM74-like GPCR polypeptide are also useful for treating the above diseases, susceptibility to diseases and abnormalities related to the correct of mutations in the nucleic acid sequences which may act as agonists or antagonists at the receptor site and which can be regulated to provide therapeutic effects. The polypeptide is also useful as a bait correction in a two-hybrid or three-hybrid assay, and to immunise a mammal correct production of polyclonal antibodies. This sequence encodes the human correct correction of provide the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated polynucleotide, useful for treating infection, pain, cancer, asthma, hypertension, myocardial infarction, urinary retention, osteoporosis, encodes the human HM74-like G-protein coupled receptor
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hyperproliferative disorder; neurological disorder; psychiatric disease;
inflammatory disorder; respiratory disorder; gene therapy; ds.
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          GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGGACAGGTATTTCAAAGTGGTCCACCCC
                                            GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
                                                                                                         TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
                                                                                                                                                                                                                 TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
                                   CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCGCACCCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene encoding novel human G protein-coupled receptor (GPCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                  1021 CACATTGTTGAGTGGCACTGA 1041
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The present invention relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor coupled receptor (GPCR) which is related to the chemokine receptor (GPCR) which is related to the chemokine receptor (GPCR) which is sequences encoding for GPCR are also given in the invention. The sequences of the invention are useful conditions mediated by human proteases. Such diseases include hyperproliferative disorders (e.g. Parkinson's disease), (e.g. parkinson's disease), (e.g. diabetes) and respiratory disorders (e.g. parkinson's disease), (e.g. diabetes) and respiratory disorders (e.g. adult respiratory disorders) (e.g. diabetes) and respiratory disorders (e.g. adult respiratory disorders) (e.g. distress syndrome, ARDS). The GPCR protein is also useful for identifying adents for use in mammalian therapeutic applications, a human drug, particularly modulating a biological or pathological response in a cell or tissue that expresses the protein, in biological casays related to GPCRs that are related to members of the chemokine receptor subfamily, in drug screening assays and in competition binding assays. GPCR is also useful in diagnosing a disease or predisposition to a disease mediated by the peptide, in pharmacogenomic analysis. The polyucleotide sequences can also be used in gene therapy. The present condition is a parking the puman GPCR gene sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                        Novel human G-protein coupled receptor proteins and nucleic acid molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the protein.
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                                                                                                                                                                                                                                                                              Francesco V,
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                                                                2000US-192419P.
2000US-230459P.
2000US-0666535.
27-MAR-2001; 2001WO-US09522
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06-SEP-2000;
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                                       TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTTGCTCCTTCAAGATTGTT
                                                                                                                      TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
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Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
                                                                                                                                                                                                                                                                                                                                                                                                      Human GPCR1c polynucleotide SEQ ID NO 4.
                                                ABA81531 standard; DNA; 1104 BP
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2000US-194614P.
2000US-195063P.
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                                                                                                                                                                                                                                                                                        (first entry)
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05-APR-2000; 2
06-APR-2000; 2
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ABA8153
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The invention relates to nucleic acid sequences (ABAB1529-ABAB152) that encode Groupled protein-receptor related polypeptides (ABB4522-ABB44543). The isolated polypeptide having a sequence differing by no more than 15 % of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the compact of sequences (or properties and entities) that can be administered therapeutically, especially using gene therapy and expressing the encoding DNA in vivo, to treat or prevent credited disorders, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atherosclerosis, disorders credated to signal processing and metabolic pathway modulation (e.g. obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disorder, Huntington's disease, neurological disorders, bacterial, fungal, protozoal and viral infections (e.g. with human (muniodeficiency virus (HTV)-1 or HTV-2). They can be used diagnostically immuned the presence of or predisposition to a disease associated with altered levels of the polypeptide expression levels especially humans) by detecting alterations in polypeptide expression levels elabeliae of control samples They are useful to identify agents binding polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGTTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and
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Li L;
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Spytek KA,
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Tchernev VT,
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06-APR-2000; 2000US-195066P.
06-APR-2000; 2000US-195067P.
06-APR-2000; 2000US-195068P.
06-APR-2000; 2000US-195070P.
06-APR-2000; 2000US-195070P.
21-JUL-2000; 2000US-221384P.
27-JUL-2000; 2000US-221384P.
28-JUL-2000; 2000US-224588P.
11-AUG-2000; 2000US-224588P.
11-OCT-2000; 2000US-224588P.
11-AUG-2000; 2000US-224588P.
11-AUG-2000; 2000US-224588P.
11-AN-2001; 2001US-265508P.
23-JAN-2001; 2001US-265508P.
23-JAN-2001; 2001US-265508P.
29-JAN-2001; 2001US-265508P.
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P-PSDB; ABB44523.
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Matches 1039; Conserv
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Padigaru M,
Baumgartner J
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         GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
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 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTACCTTTTCAATTTGGCCGTGGCT
                                                                             TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
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DNA; 888

AAH50974 standard;

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RESULT 10 AAH50974 AAH50974;

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28-AUG-2001 (first entry)

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The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

28, 31-38, 40, 41, 53-60) and their coding sequences. The present

c sequence is the coding sequence for one such G protein-coupled receptor.

GFCRs are also known as seven transmembrane receptors and function in

sequences are useful for

GFCRs are also known as seven transmembrane receptors and function in

c signal transduction. The nGPCRx coding sequences are useful for

c screening a human to diagnose a disorder affecting the brain or a genetic

c dentifying compounds useful for treating schizophrenia. Detection of

c nGFCRx in a sample is useful as a diagnostic tool for diseases or

c disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,

c disorders, infections such as HIV-1, metabolic and cardiovascular

c disorders, infections such as HIV-1, metabolic and cardiovascular

c disorders, infections such as and hormonal disorders, wodulators of

c nGPCRx activity have the utility for treating neurological disorders,

c nGPCRx activity have the utility for treating neurological disorders,

c nGPCRx activity have the utility for treating neurological disorders,

c nGPCRx activity have the utility for treating neurological disorders,

c nGPCRx activity have the utility for treating neurological disorders,

c nGPCRx activity have the utility for treating neurological disorders,

c disease, proliferation deficit disorder, and neuronal disorders such as

Additional disorders include inflammatory conditions (e.g. Crohn's

c disease), rheumatoid arthritis, autoimmune disorders, cancers,

c negpliatory allments such as asthma, and inflammatory diseases e.g.

inflammatory bowel disease.
                                                                      signal transduction; schizophrenia, thyroid disorder; renal failure, rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neurological disorder; neurological disorder; partention deficit-hyperactivity disorder/attention deficit disorder; parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autolmmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                         receptor;
enal failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nd P, Slightom J;
Sejlitz T, Huff
                                                         seven transmembrane
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V, Sejlit
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an CM, Ruff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 77; 261pp; English.
                Human nGPCR11 coding sequence #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PHAA ) PHARMACIA & UPJOHN CO.
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2000US-018B114.
2000US-0190310.
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2000US-0185554.
2000US-0186530.
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99US-0166678.
99US-0173396.
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                                                         protein-coupled receptor;
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2000US-0201190
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                                                                                                                                                                                                                  neuroprotective; ds
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02-MAR-2000;
03-MAR-2000;
09-MAR-2000;
17-MAR-2000;
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02-MAY-2000;
08-MAY-2000;
                                                                                                                                                                                                                                                         Homo sapiens.
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19-NOV-1999;
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hRUP25. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
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                                                                                Human; G-protein coupled receptor; GPCR; hRUP25; agonist;
inverse agonist; lung cancer; ss.
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                                           encoding G-protein coupled receptor,
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                                                                                                                                                                                      Location/Qualifiers
1..1092
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2000US-0203630.
2000US-0210741.
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20000S-0235779.
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99US-0166369.
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(first entry)
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                                                                                                                                                                                                                                 /*tag=
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P-PSDB; AAU04379.
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  23-OCT-2001
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23-DEC-1999;
23-DEC-1999;
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                                                                                                                         CTGCTCATTGTGGCCTTTGTGCTGGGCGCCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
                                                                                                                                                                                                            TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180
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                                                                                    Gaps
                                                                                                                                               GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
                                                                                                                                                                                                                                                                                                                                                                            241 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAGCATCGTGTTCCTTACGGTGGTGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
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                                                                                  Indels
                                         Length
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                                         DB 22;
                          standard; cDNA; 1092
                                                                                    Conservative
                                       Query Match
Best Local Similarity
Matches 888; Conserv
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AAS07952

790 CTCAGCTTCACCTACATGAACAGCATGCTGGA 821

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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90663-AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 and AAAA30779-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TW6 to form a sequence X-(AA)15-pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stratch between the substituted amino acid and the Promay be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous, or a mixture of endogenous and non-endogenous, non-endogenous, or a mixture of endogenous and non-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research and account of the receptors in normal and account of the receptors in ormal account of the receptors in ormal and account of the receptors in ormal and account of the receptors in ormal account of the receptors and account of the receptors and account of the receptors and account of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human G protein-coupled receptor HM74 cDNA.
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Example 1; Page 185; 341pp; English.
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                                                                                                                                                                                                                                                                                                                                                     AAA30658 standard; cDNA; 1164 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-329165/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L3-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA30658;
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                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                   AAA30658
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAAY90677 and AAAY90677 and AAAY90677 and AAAY9079). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (TS3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, x, is substituted for an endogenous proline in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X (AAA)15-pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The IS amino acid stretch between the substituted and the Promay be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as cettings for elucidating the roles of the receptors in normal and settings for elucidating the roles of the receptors in normal and consequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAA30709- AAA30743 and AAA30775-A30779 represent DNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                        DNA encoding human mutant G protein-coupled receptor HM74 (1230K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.1%; Score 32; DB 21; Length 1164; Best Local Similarity 100.0%; Pred. No. 8.9e-06; Matches 32; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1164 BP; 248 A; 335 C; 289 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding the mutant human GPCRs of the invention.
838 CTCAGCTTCACCTACATGAACAGCATGCTGGA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 285-286; 341pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liaw CW;
                                                                                                                                                                                                                                                                                                                    intracellular loop 3; transmembr
agonist; antagonist; mutant; ss.
                                                                                                                         AAA30738 standard; DNA; 1164 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US23938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0170496
                                                                                                                                                                                                              21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Behan DP, Chalmers DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-329165/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200022129-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                    AAA30738;
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Gaps

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3.1%; Score 32; DB 21; Length 1164; 100.0%; Pred. No. 8.9e-06; tive 0; Mismatches 0; Indels C

Query Match 3.1% Best Local Similarity 100.( Matches 32; Conservative

(first entry)

CTCAGCTTCACCTACATGAACAGCATGCTGGA 821

790

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AAH51053 standard; DNA; 24 BP.
                                                                                                                                          Oligonucleotide SEQ ID 133.
                                                                                                            28-AUG-2001
                                                                            AAH51053;
               RESULT 15
                              AAH51053
                                                             The present sequence encodes a member of the G-protein coupled receptor (7TM receptor) family, designated the HM74A receptor. The proteins, agonists, antagonists and polynucleotides can be used for treating disorders associated with increased or reduced expression or activity of insorders associated with increased or reduced expression or activity of HM74A, e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HW-1 or HW-2, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, actue heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, mand depression, debression, delirium, dementia, and severe mental retardation, and dyskinesias such as Huntington's disease or cliles de la Tourett's syndrome. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                         HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated G-protein coupled receptor, HM74A - used to develop products for treating e.g. infections, pain, cancers, diabetes, obesity, neurological disorders, heart failure, hypertension, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mooney JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 20; I
Pred. No. 8.9e-06;
                                                                                                                                                                                         G-protein coupled receptor HM74A encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.1%; Scor.
100.0%; Pred. No. c.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "HM74A receptor"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 30-31; 40pp; English.
                                                                                           AAX16671 standard; cDNA; 1361 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0049480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US12386
                                                                                                                                                           29-APR-1999 (first entry)
                                                                                                                                                                                                                                                         asthma; allergy; ss.
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                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-1998
                                                                                                                           AAX16671;
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             838
                                                             RESULT 14
                                                                            AAX1667]
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The present invention relates to novel G protein-coupled receptors (nGPCRX; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 57-60) and their coding sequences (see AAH50049-AAH51015 and AAAG80929-AAG80975 and AAG80977. The present sequence is an oligonucleotide, which was used in the present invention. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful conscreening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders. renal failure, rheumatoid arthitis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of
G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrania; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder/attention deficit disorder; parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parodi LA, Hiebsch RR, Lind P, Slightom J;
PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 246; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PHAA ) PHARMACIA & UPJOHN CO.
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2000US-0185554.
2000US-0186530.
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99US-0166678.
99US-0173396.
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2000US-0201190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-389826/41.
                                                                                                                                                                                                                                                                                                neuroprotective; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200136473-A2.
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28-FEB-2000; 2
02-MAR-2000; 2
03-MAR-2000; 2
09-MAR-2000; 2
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28-DEC-1999;
22-FEB-2000;
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02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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Gaps

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0; Indels

898 CTCAGCTTCACCTACATGAACAGCATGCTGGA 929

CTCAGCTTCACCTACATGAACAGCATGCTGGA 821

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Matches 32; Conservative

Local Similarity

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nCPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; carcer; attention deficit-hyperactivity disorder; Alzheimer's disease; cancer; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lind P, Slightom J; ... collitz T, Huff RM;
                                                                                                                                                                                                Gaps
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                                                                                                                                                               Score 24; DB 22; Length 24;
Pred. No. 0.094;
0; Mismatches 0; Indels
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                                                                                                                                    Sequence 24 BP; 3 A; 7 C; 5 G; 9 T; 0 other;
                                                                                                                                                                          100.0%; Pred. wc.
                                                                                                                                                                                                                        707 GCGTGTCTGCTAGACTCTATTTCC 730
                                                                                                                                                                                                                                      1 GCGTGTCTGCTAGACTCTATTTCC 24
                                                                                                                                                                                                                                                                                                                                                                                                                    Human nGPCR11 PCR primer LW1660.
                                                                                                                                                                                                                                                                                                                            AAH51082 standard; DNA; 24 BP.
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99US-0166678.
99US-0173396.
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2000US-0186530.
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09-MAR-2000; 2000US-0188114.
17-MAR-2000; 2000US-0190310.
21-MAR-2000; 2000US-0190800.
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2000US-0201190.
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                                                                                                      inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2001 (first entry)
                                                                                                                                                                            Local Similarity 100.
nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-389826/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-2000;
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28-DEC-1999;
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                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                         AAH51082;
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                 RESULT 16
                                                                                                                                                                                                                                                                                                                AAH51082
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New G protein-coupled receptor (nGPCR-x) and its encoding

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The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see 28, 31-38, 40, 41, 53-60) and their coding sequences (see present sequence is a PCR primer, which was used in an example from the present invention GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for Identifying compounds useful for treating schizophrenia.

Or a genetic predisposition, specifically schizophrenia nGPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-disorders, including schizophrenia, ADHD/ADD (attention deficit-disorders, such as Alzheimer's disease, magraine and carcing dementia, additional disorders include inflammatory conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; autoimmune disorder; respiratory ailment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%; Score 24; DB 22; Length 24; 100.0%; Pred. No. 0.094; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 3 A; 7 C; 5 G; 9 T; 0 other;
                                       Example 11; Page 143; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707 GCGTGTCTGCTAGACTCTATTTCC 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .g. inflammatory bowel disease.
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990S-0166678.
990S-0173396.
2000US-018421.
2000US-018554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective; ss
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17-NOV-1999;
19-NOV-1999;
28-DEC-1999;
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28-FEB-2000;
28-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH51050;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 17
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New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                od LS, Parodi LA, Hiebsch RR, Lind P, Slight
Raytes PS, Bannigan CM, Ruff V, Sejlitz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 11; Page 143; 261pp; English.
              neuroprotective; PCR primer; ss
                                                                                                                                                                        16-NOV-1999; 99US-0165838.
17-NOV-1999; 99US-0166071.
28-DEC-1999; 99US-0166678.
22-FEB-2000; 2000US-0184129.
28-FEB-2000; 2000US-0184129.
28-FEB-2000; 2000US-018554.
02-MAR-2000; 2000US-0186530.
03-MAR-2000; 2000US-0186530.
09-MAR-2000; 2000US-018611.
09-MAR-2000; 2000US-018611.
17-MAR-2000; 2000US-0186114.
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                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000; 2000US-0190800.
20-APR-2000; 2000US-0198568.
02-MAY-2000; 2000US-0201190.
08-MAY-2000; 2000US-0203111.
                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000; 2000US-0207094
                                                                                                                                               2000WO-US31581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-389826/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood LS,
                                                                              WO200136473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vogeli G, Woc
Schellin KA,
                                                Homo sapiens.
                                                                                                             25-MAY-2001,
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                present sequence is an oligonucleotide, which was used in the present invention. GPCRs are also known as seven transmembrane receptors and invention in signal transduction. The indeptx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of inclentifying compounds useful for treating schizophrenia. Detection of disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular disorders, infections such as HIV-1, metabolic and cardiovascular including schizophrenia, ADHD/ADD (attention deficit-hyperactivity including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorders parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel G protein-coupled receptors (nGPCRX; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH50059-AAH51015 and AAH51105 and AAG80929-AAG80975 and AAG80977). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; achizophrania; hyproid disorder; renal failure; rhematoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neuronal disorder; attention deficit-hyperactivity disorder/attention deficit disorder; parklnson's disease; mancer; parklnson's disease; magraine; senile dementia; inflammatory disease;
                                                                                                                                                                                           od LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                          New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            respiratory ailments such as asthma, and inflammatory diseases e.g.
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Pred. No. 0.093;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 52 BP; 12 A; 14 C; 12 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 2.3%; Score 24; DB Local Similarity 100.0%; Pred. No. 0.C es 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                        Disclosure; Page 245; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGTGTCTGCTAGACTCTATTTCC 730
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                                                                                                                                                              (PHAA ) PHARMACIA & UPJOHN CO
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                                              2000US-0190310.
2000US-0190800.
2000US-0198568.
2000US-0201190.
                                                                                                            08-MAY-2000; 2000US-0203111.
25-MAY-2000; 2000US-0207094.
              2000US-0186811
2000US-0188114
 2000US-0186530
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                                                                                                                                                                                                                                            WPI; 2001-389826/41.
                                                                                                                                                                                             Wood LS,
                                                                                                                                                                                           Vogeli G, Woc
Schellin KA,
                                            17-MAR-2000;
21-MAR-2000;
20-APR-2000;
02-MAY-2000;
                                 09-MAR-2000;
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Matches
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Slightom J; fz T. Huff RM;

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The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH51015 and AAH51059-AAG80975 and AAG80977). The present sequence is a PCR primer, which was used in an example from the present invention. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia.

Or a genetic predisposition, specifically schizophrenia chickenses or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders including schizophrenia, AAHD/ADD (attention deficit-chiperactivity disorder/attention deficit disorders und neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and cannot be an additional disorders includers and processes an expense of the conditions and disorders includers and disorders includers and an enronal disorders and demential disorders includers and disorders includers and hormonal disorders and demential disorders includers and hormonal disorders includers and hormonal disorders and hormonal disorders includers and hormonal disorders and the demential disorders includers and hormonal disorders and the demential disorders includers and distince and disorders and hormonal disorders and the demential disorders and disparse and d
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cancers, respiratory ailments such as asthma, and inflammatory diseases
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Pred. No. 0.093;
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH51015 and AAH51105 and AAG80929-AAG80975 and AAG80977). The
                                                                                                                                                                                                      signal transduction, schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; hormonal disorder; attention deficit-hyperactivity disorder/attention deficit disorder; partention deficit disorder; rheumatoid arthritis; autoimmune disorder; respiratory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
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Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff
                                                                                                                                                                                           G protein-coupled receptor; nGPCR; seven transmembrane receptor;
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                                                                                                                                                        Human nGPCR11 PCR primer LW1565.
                                                AAH51029 standard; DNA; 33 BP
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99US-0166678.
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2000US-0185421.
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2000US-0198568
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                                                                                                                     (first entry)
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22-FEB-2000;
28-FEB-2000;
02-MAR-2000;
03-MAR-2000;
04-MAR-2000;
17-MAR-2000;
21-MAR-2000;
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08-MAY-2000;
                                                                                                                     28-AUG-2001
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                                                                                   AAH51029;
                RESULT 19
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disorders, including schizophrenia, ADHD/ADD (attention deficithyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autolumnune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signal transduction; schizophrenia, thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; attention deficit-hyperactivity disorder/attention deficit disorder; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory disease; neuroprotective; PCR primer; se.
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PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                      0; Indels
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28-FEB-2000; 2000US-0185421.
28-FEB-2000; 2000US-018554.
02-MAR-2000; 2000US-018554.
09-MAR-2000; 2000US-0186811.
17-MAR-2000; 2000US-0188114.
17-MAR-2000; 2000US-0190800.
21-MAR-2000; 2000US-0190800.
20-MAR-2000; 2000US-0190800.
21-MAR-2000; 2000US-0190800.
02-MAY-2000; 2000US-0201190.
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99US-0166678.
99US-0173396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH51028 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                               Query Match 2.2%
Best Local Similarity 100.(
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200136473-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001
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AAH51031;
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            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

28, 31-38, 40, 41, 53-60) and their coding sequences (see
ANH50869-AAH51015 and AAH5105 and AAG80929-AAG80975 and AAG80977). The
present sequence is a PCR primer, which was used in an example from the
present invention. GPCRs are also known as seven transmembrane receptors
and function in signal transduction. The nGPCRx coding sequences are
useful for screening a human to diagnose a disorder affecting the brain
cor a genetic predisposition, specifically schizophrenia. nGPCRx are
useful for identifying compounds useful for treating schizophrenia.

Cor a genetic conferex in a sample is useful as a diagnostic tool for
the preses or disorders e.g. thyroid disorders, renal failure, rheumatoid
arthritis, CNS disorders, infections such as HIV1, metabolic and
cardiovascular diseases, proliferative disorders and hormonal disorders.

Modulators of nGPCRx activity have the utility for treating neurological
disorders, including schizophrenia, AHDADD (attention deficit.
hyperactivity disorder/attention deficit disorder, and neuronal
cardiovascular disease, proliferative disorder, and neuronal
disorders such as Alzheimer's disease, Parkinson's disease, migraine and
senie dementia. Additional disorders include inflammatory conditions
cancers, respiratory ailments such as asthma, and inflammatory diseases
e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit hyperactivity disorder/attention deficit disorder; Parkinson's disease; migralne; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33 BP; 7 A; 9 C; 9 G; 8 T; 0 other;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                    Example 2; Page 101; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.00,
100.0%; Pre-
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH51030 standard; DNA; 20 BP
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99US-0166071.
99US-016678.
99US-0173396.
2000US-0184129.
2000US-018554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-2000; 2000WO-US31581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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28-FEB-2000;
02-MAR-2000;
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28-DEC-1999;
22-FEB-2000;
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\overset{\mathsf{x}}{\mathsf{a}}\overset{\mathsf{x}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\mathsf{o}}}\overset{\mathsf{o}}{\mathsf{o}}\overset{\mathsf{o}}{\maths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The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41,53-60) and their coding sequences (see 28, 31-38, 40, 44)5105 and their coding sequences (see present sequence is a PCR primer, which was used in an example from the present sequence is a PCR primer, which was used in an example from the present invention. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a thran to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia.

Or a genetic predisposition, specifically schizophrenia checking the brain or nGPCRx in a sample is useful a a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthitis, CRS disperser; infections such as HIV1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-disorders, understance and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile demential disorders includes and neuronal disorders includes employed the inclusions of senile demential disorders includes and neuronal disorders includes employed the inclusions and neuronal disorders includes and an entities are a protein and present and an entity of the present and pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratoja valuents such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neurological disorder; neurol defibit hyperactivity disorder; Alzheimer's disease; cancer; attention defibit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         di LA, Hiebsch RR, Lind P, Slightom J;
Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parodi LA,
                                                                                                                                                                                                                                                                                                                                                                                                          UPJOHN CO
                                                                              17-MAR-2000; 2000US-0190310.
21-MAR-2000; 2000US-0190800.
20-AAR-2000; 2000US-0198568.
02-MAY-2000; 2000US-0201190.
08-MAY-2000; 2000US-0201190.
25-MAY-2000; 2000US-0207094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood LS,
A, Kaytes
20000S-
20000S-
20000S-
20000S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 117
                                                                                                                                                                                                                                                                                                                                                                                                          (PHAA ) PHARMACIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-389826/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vogeli G, Woo
Schellin KA,
                                         09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001
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G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;

neuroprotective; ss

WO200136473-A2.

Synthetic.

25-MAY-2001

AAH51051 standard; DNA; 20 BP.

Oligonucleotide SEQ ID 131

(first entry)

28-AUG-2001

AAH51051;

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AAH51051,
                                                                     The present invention relates to novel G protein-coupled receptors

(nGPCRX: where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
28, 31-38, 40, 41, 53-60) and their coding sequences (see
28, 31-38, 40, 41, 53-60) and their coding sequences (see
present sequence is a PCR primer, which was used in an example from the
present invention. GPCRs are also known as seven transmembrane receptors
and function in signal transduction. The nGPCRx coding sequences are
useful for screening a human to diagnose a disorder affecting the brain
or a genetic predisposition, specifically schizophrenia. nGPCRx are
useful for identifying compounds useful for treating schizophrenia.
Detection of nGPCRx in a sample is useful as a diagnostic tool for
diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid
arthritis, CNS disorders, infections such as HIV1, metabolic and
cardiovascular diseases, proliferative disorders and hormonal disorders.
Modulators of nGPCRx activity have the utility for treating neurological
disorders und schizophrenia, ADHD/ADD (attention deficit-
disorders such as Alzheimer's disease, Parkinson's disease, migraine and
senile dementia. Additional disorders include inflammatory conditions
(e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders,
cancers, respiratory aliments such as asthma, and inflammatory diseases
e.g. inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parodi LA, Hiebsch RR, Lind P, Slightom J;
PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 117; 261pp; English.
neuroprotective; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                          2000US-0184129
2000US-0185421
                                                                                                                                                                                                                                                                                            02-MAR-2000; 2000US-0186530
                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000; 2000US-0190800
20-APR-2000; 2000US-0198568
02-MAY-2000; 2000US-0201190.
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                                                                                                                                      2000WO-US31581
                                                                                                                                                                                         99US-0166071
99US-0166678
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                                                                                                                                                                                                                                                                                                              2000US-0186811
                                                                                                                                                                                                                                                                                                                              2000US-0188114
                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0203111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-389826/41.
                                                                   WO200136473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schellin KA,
                                                                                                                                                                                                                                                                                                          03-MAR-2000;
09-MAR-2000;
                                     Homo sapiens.
                                                                                                                                      16-NOV-2000;
                                                                                                                                                                                                                                                        28-FEB-2000;
28-FEB-2000;
                                                                                                                                                                                                                                                                                                                                              17-MAR-2000;
                                                                                                                                                                                                                                          22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2000;
                                                                                                                                                                                                        19-NOV-1999;
28-DEC-1999;
                                                                                                    25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vogeli G,
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2000US-0185421. 2000US-0185554. 2000US-0186530.

28-FEB-2000; 02-MAR-2000;

2000US-0184129

17-NOV-1999; 19-NOV-1999; 28-DEC-1999; 22-FEB-2000; 28-FEB-2000;

16-NOV-2000; 2000WO-US31581

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present sequence is an oligonouteotide, which was used in the present invention. GPCRs are also known as seven transmembrane receptors and invention. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity
                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel G protein-coupled receptors (nGPCRX; where x is 1, 3, 4, 5, 9, 11, 12, 1418, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAHS1015 and AAHS1105 and AAG80929-AAG80975 and AAG80977). The
                                                                                                                   New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                      Disclosure; Page 245; 261pp; English.
WPI; 2001-389826/41
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Gaps

ö

0; Indels

0; Mismatches

100.08;

20; Conservative

Local Similarity

Query Match Matches 327 GGCTGCGGACAGGTATTTCA 346

õ a

20 GGCTGCGGACAGGTATTTCA 1

1.9%; Score 20; DB 22; Length 20; 100.0%; Pred. No. 9.4;

Parodi LA, Hiebsch RR, Lind P, Slightom J; PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;

(PHAA ) PHARMACIA & UPJOHN CO

Kaytes Wood LS,

Schellin KA,

Vogeli G,

2000US-0198568. 2000US-0201190. 2000US-0203111.

2000US-0207094

2000US-0190310

03-MAR-2000; 09-MAR-2000; 17-MAR-2000; 21-MAR-2000;

20-APR-2000; 02-MAY-2000; 08-MAY-2000; 25-MAY-2000;

2000US-0186811 2000US-0188114 2000US-0190800 us-09-886-041-1.olig.rng

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Example 11; Page 143; 261pp; English.
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irc}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}
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                         Alzhelmer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory aliments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal transduction; schizophrenia; thyroid disorder; renal failure; rhemmatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder/attention deficit disorder parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
disorder/attention deficit disorder), and neuronal disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il LA, Hiebsch RR, Lind P, Slightom J;
Bannigan CM, Ruff V, Sejlitz T, Huff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-coupled receptor; nGPCR; seven transmembrane receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                    Score 20; DB 22; Length 20; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                       Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human nGPCR11 PCR primer LW1661.
                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.9%; Scc
Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        od LS, Parodi LA,
Kaytes PS, Bannig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        962 GGAGTTGCATCAGTGTGGCA 981
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2000US-0184129.
2000US-0185421.
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2000US-0186530.
2000US-0186811.
2000US-0188114.
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2000US-0198568.
2000US-0201190.
2000US-0203111.
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99US-0166678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0207094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200136473-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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28-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH51080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH51080,
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The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

(28, 31-38, 40, 41, 53-60) and their coding sequences (see

28, 31-38, 40, 41, 53-60) and their coding sequences (see

present sequence is a PCR primer, which was used in an example from the

present invention. GPCRs are also known as seven transmembrane receptors

and function in signal transduction. The nGPCRx coding sequences are

useful for screening a human to diagnose a disorder affecting the brain

or a genetic predisposition, specifically schizophrenia. nGPCRx are

useful for identifying compounds useful for treating schizophrenia.

Detection of nGPCRx in a sample is useful as a diagnostic tool for

disposases or disorders e.g. thyroid disorders, renal failure, rheumatoid

ardiovascular diseases, proliferative disorders and hormonal disorders.

Modulators of nGPCRx activity have the utility for treating neurological

disorders uch as Alzheimer's disease, Parkinson's disease, migraine and

senila dementia. Additional disorders, including schizophrenia, ADHD/ADD (attention deficit

hyperactivity disorder/attention deficit disorder, and neuronal

disorders such as Alzheimer's disease, parkinson's disease, migraine and

senila dementia. Additional disorders including inflammatory conditions

(e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders,

cancers, respiratory allments such as asthma, and inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20; DB 22;
Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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100.0%; Pic
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH51052 standard; DNA; 48 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       990S-0165838.
990S-0166771.
990S-016678.
990S-0173396.
2000US-0184129.
2000US-018554.
2000US-0186530.
2000US-0186530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 GGAGTTGCATCAGTGTGGCA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-NOV-2000; 2000WO-US31581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide SEQ ID 132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200136473-A2.
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22-FEB-2000;
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03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000;
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19-NOV-1999;
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Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
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                                                                                         16-NOV-2000; 2000WO-US31581
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-389826/41.
                                       WO200136473-A2.
                                                                                                                                                                                            28-FEB-2000;
02-MAR-2000;
03-MAR-2000;
                 Homo sapiens.
                                                                                                                                                                                                                                  09-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                            21-MAR-2000;
                                                                                                                                                                                                                                                                                     02-MAY-2000;
                                                                                                                                                                                                                                                                                                               25-MAY-2000;
                                                                                                                                                                                28-FEB-2000;
                                                                                                                                                                                                                                                                       20-APR-2000
                                                                 25-MAY-2001
     The present invention relates to novel G protein-coupled receptors (GPCRX: where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH50968-AAH51015 and AAH51015 and AAG80929-AAG80975 and AAG80977). The present sequence is an oligonucleotide, which was used in the present invention. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful for treating schizophrenia. Detection of nGPCRx in sample is useful as a diagnostic tool for diseases or disorders infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders, and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, include inflammatory conditions (e.g. Crohn's disease), rheumatoid efficit disorder) conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory aliments such as asthma, and inflammatory diseases e.g.
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                                                                                                                              Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                           New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor; nGPCR; seven transmembrane receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48 BP; 14 A; 15 C; 10 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
                                                                                                                                                                                                                               Disclosure; Page 246; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human nGPCR11 PCR primer LW1659.
                                                                                                     (PHAA ) PHARMACIA & UPJOHN CO.
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ID AAH51081 standard; DNA; 48 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  962 GGAGTTGCATCAGTGTGGCA 981
                                     20-APR-2000; 2000US-0198568.
02-MAY-2000; 2000US-0201190.
08-MAY-2000; 2000US-0203111.
25-MAY-2000; 2000US-0207094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 GGAGTTGCATCAGTGTGGCA 29
                         2000US-0190800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                   WPI; 2001-389826/41
09-MAR-2000;
17-MAR-2000;
21-MAR-2000;
                                                                                                                            Vogeli G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH51081;
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2000US-0185554. 2000US-0186530. 2000US-0186811.

2000US-0184129

2000US-0185421

2000US-0188114, 2000US-0190310,

2000US-0201190 2000US-0190800

2000US-0198568

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                                                                                                                                                                                                               The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH51045 and AAH51115 and AAH51115 and AAH51105 and AAG80975 and AAG80977). The present sequence is a PCR primer, which was used in an example from the present invention. GPCRs are also known as seven transmembrane receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthitis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-
New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schlzophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48 BP; 14 A; 15 C; 10 G; 9 T; 0 other;
                                                                                                                              Example 11; Page 143; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       962 GGAGTTGCATCAGTGTGGCA 981
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Best Local Similarity 100.(
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RESULT 27

signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; saccinity disorder/attention deficit disorder; parkinson's disease; migralne; senile dementia; inflammatory disease; rheumatoid arthritis; autolimence disorder; respiratory ailment; neuroprotective; PCR primer; ss.

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2000US-0232081.
2000US-0232398.
2000US-0232399.
2000US-0232399.
2000US-0232400.
2000US-0232400.
2000US-0232400.
2000US-023423964.
2000US-02344997.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-0236844.
2000US-0236834.
2000US-0236834.
2000US-0236834.
2000US-0236834.
2000US-0236836.
2000US-0236836.
2000US-0236836.
2000US-0236889.
2000US-0236889.
2000US-0236889.
2000US-0236889.
2000US-0236889.
2000US-0236889.
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20000S - 0241786

20000S - 0241809

20000S - 0241809

20000S - 0246174

20000S - 0246474

20000S - 0246477

20000S - 0246477

20000S - 0246477

20000S - 0246528

20000S - 0246527

20000S - 0246528

20000S - 0246610

20000S - 0246611

20000S - 0246238

20000S - 0249208

20000S - 0249218

20000S - 0249218
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20000S-0239937.
20000S-0240960.
20000S-0241221.
      2000US-0232080
 08 - SEP - 2000; 20 - S
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17 - NOV - 2000;
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17-NOV-2000;
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      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vinerary; anticonvulsant; antibacterial; antifungal; antiparaaitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                                                                                         Human musculoskeletal system related polynucleotide SEQ ID NO 3513.
AAL37148/c
ID AAL37148 standard; DNA; 4715 BP.
                                                                                                                                                                                                                                                                                                                                                            2000US - 0179065
2000US - 0186528
2000US - 0186350
2000US - 0186350
2000US - 0198123
2000US - 0198123
2000US - 0129467
2000US - 0129467
2000US - 0118296
2000US - 0125214
2000US - 0125266
2000US - 0125268
2000US - 0125268
2000US - 0125757
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2000US - 0126186
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2000US-0231242.
2000US-0231243.
2000US-0231413.
2000US-0231413.
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                                                                           (first entry)
                                                                                                                                                                                                                                                                      WO200155367-A1
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04-FEB-2000;
02-FEB-2000;
02-MAR-2000;
11-MAR-2000;
11-MAR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
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06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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18-AUG-2000;
22-AUG-2000;
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                                              AAL37148
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Myers

Li PWD,

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capable of detecting 1000 or more genes from prosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLiG176-ABL3051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                  claim 1; SEQ ID NO 2656; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 912 BP; 265 A; 188 C; 225 G; 234 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            805 ATGAACAGCATGCTGGATC 823
                                                                                                          23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
hes 19; Conservative
                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                       WPI; 2001-656860/75
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                                                                                                                                                           (PEKE ) PE CORP NY.
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                WO200171042-A2.
                                                                                                                                                                                                                                                                                      interactions
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                                            27-SEP-2001
                                                                                                                                                                                        Venter JC,
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ABL02109/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB3087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti-agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, lung, or urogenital; (b) immune consenses e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and (f) infectious diseases such as viral, backers..., parasitic infections.

Parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.Wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
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100.0%; Pred. No. 9;
tive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                      Barash SC, Ruben SM;
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ID ABL17061 standard; DNA; 912 BP
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                                                                                                                         08-DEC-2000; 2000US-0251868.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251989.

08-DEC-2000; 2000US-0251990.

11-DEC-2000; 2000US-0259678.
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                          2000US-0250391.
2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0256719.
                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                          2000US-0251856
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                                       05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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                                                                                                                                                                                                                                                                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                 diagnosis
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Gaps

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Indels

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0; Mismatches

100.08;

1.8%; Score 19; DB 23; Length 912; 100.0%; Pred. No. 29;

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developmental biology; cell signalling; insecticide;
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                                                                                                                                            BP.
                                                                                                                                       ABL02109 standard; cDNA; 2947
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11-JUL-2000; 2000US-0614150.
41 ATGAACAGCATGCTGGATC 23
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                                                                                                                                                                                                                                                                                                                                                              pharmaceutical; gene; ss
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Gaps

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0; Indels

Score 19; DB 23; Pred. No. 29; 0; Mismatches 0

Length 2977;

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 9727.
                                                                                               Sequence 2977 BP; 845 A; 616 C; 680 G; 836 T; 0 other;
                                                                                                                                                                                                                                                                          418/c
ABL19418 standard; DNA; 3482 BP.
                                                                                                                           Query Match 1.8%; Soc
Best Local Similarity 100.0%; P.
Matches 19; Conservative 0;
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 100.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical; gene; ds
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                sequences (ABL01840-P) (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                  ABL19418;
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                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLiol76-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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0
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                                                                                                                                                                                                                                                                                                                               23; Length 2947;
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                                                                                              Claim 1; SEQ ID NO 809; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                   Sequence 2947 BP; 772 A; 921 C; 719 G; 535 T; 0 other;
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100.0%; Pre
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ID ABL17060 standard; DNA; 2977
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                  sequences (ABL01840-A
(ABB57737-ABB72072).
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WPI; 2001-656860/75.
P-PSDB; ABB58006.
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                                                                      interactions
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Matches
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLLG176-ABL30511), expressed DNA sequences (ABLG176-ABL30511), expressed DNA
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100.0%; Pred. No. 28;
ive 0; Mismatches
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Myers EW;

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2000US-0241787.
2000US-0241808.
2000US-0241809.
2000US-024617.
2000US-0246474.
2000US-0246476.
2000US-0246477.
2000US-0246477.
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2000US-0231243.
2000US-0231244.
2000US-0231414.
2000US-0232080.
2000US-0232080.
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200005-0232397.
200005-0232399.
200005-0232390.
200005-0232401.
200005-0233401.
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2000US-0233065.
2000US-0234223.
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2000US-0234997.
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2000US-0235484.
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2000US-0235836.
2000US-0236327.
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2000US-0236369.
2000US-0236370.
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2000US-0237037.
2000US-0237038.
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2000US-0239935.
2000US-0239937.
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2000US-0246525.
2000US-0246526.
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2000US-0246528.
2000US-0246532.
2000US-0246609.
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2000US-0246611.
2000US-0246613.
2000US-024503.
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2000US-0241786.
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
14-SEP-2000;
15-SEP-2000;
16-SEP-2000;
17-SEP-2000;
17-SEP-2000;
18-SEP-2000;
19-SEP-2000;
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02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
01-NOV-2000;
08-NOV-2000;
  Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antilnflammatory; anti-HIV; antibacterial; antilnflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis; or blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardlovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ds; acquired immune deficiency syndrome.
                                                                                                                         DNA encoding novel signal transduction pathway protein, Seq ID 1482
                                                            AAS27822 standard; DNA; 10098 BP
3212 ATGAACAGCATGCTGGATC 3194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0224518
2000US-0224519
2000US-0225213
2000US-0225264
2000US-0225267
2000US-0225267
2000US-0225477
2000US-0225757
2000US-0225757
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2000US-0229345
                                                                                                     07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                  WO200154733-A1
                                                                                                                                                                                                                                                                                                                                               31-JAN-2000;
04-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
19-MAY-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
14-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                               Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                       02-AUG-2001.
                                                                                 AAS27822;
                                       RESULT 3:
AAS27822
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Low density lipoprotein binding protein 1; LBP-1; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; dlagnosis;
                                          Human low density lipoprotein binding protein 1 (LBP-1) gene.
                                                                                                                                                                                                                                                                                                                                                                                (BOST-) BOSTON HEART FOUND INC.
                                                                                                                                                                                                                                                                                                                                     28-FEB-2001; 2001WO-US06356.
                                                                                                                                                                                                                                                                                                                                                     02-MAR-2000; 2000US-0517849
14-JUL-2000; 2000US-0616289
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-565505/63.
P-PSDB; AAB82802.
                                                                                                                                                                                                                                                                                                                                                                                                 Lees AM, Lees RS,
                                                                                                                                                                                                                                                                                                   WO200164874-A2.
                                                                                              Homo sapiens.
                        12-NOV-2001
                                                                             vaccine; ds.
                                                                                                                                                                                                                                                                                                                   07-SEP-2001.
        AAH26493;
                                                                                                                                                                                                                                                         intron
                                                                                                                                                                    intron
                                                                                                                                                                                                              intron
                                                                                                                                                   exon
                                                                                                                                                                                             exon
                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                           exon
Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 19; DB 22; Length 10098; 00.0%; Pred. No. 28; ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10098 BP; 2736 A; 2022 C; 1904 G; 3436 T; 0 other;
                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 1482; 880pp; English.
                                                                                                                                                                                                                               Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                            2001US-025967B.
                                                                            2000US-0249300,
2000US-0250160,
                         2000US-0249244
                                                                     2000US-0249299
                                                                                                                2000US-0251988
                                                                                                                        2000US-0256719
                                                                                                                                 2000US-0251479
                                                                                                                                                   2000US-0251868
                                                           2000US-0249297
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                               WPI; 2001-465460/50.
                                                                          17 NOV - 2000
01 - DEC - 2000
01 - DEC - 2000
05 - DEC - 2000
05 - DEC - 2000
06 - DEC - 2000
08 - DEC - 2000
                                                                                                                                                                                           05-JAN-2001;
                                  17-NOV-2000;
17-NOV-2000;
                                                   L7 - NOV - 2000;
                                                          17-NOV-2000;
                                                                     -NOV-2000;
                         .7-NOV-2000
                                                                                                                                                                           08-DEC-2000
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/cons\_splice= "(5'site:No, 3'site:No)" 5382.:5453 /\*tag= d 5454..7897

/anticodon- "8075..10902 /\*tag- 9 10903..10965

7898..8074 \*tag= \*tag=

/\*tag= a /note= "includes introns" 2875..3018

b .19..5381 /\*tag= r 'cons

Location/Qualifiers 2875..10965

(first entry)

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The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 1 (LBP-1, see AAB82802).

Conversity lipoprotein binding protein 1 (LBP-1, see AAB82802).

Convention that encode novel polypeptides, termed spans 4 exons. Human LBP-1 nucleic acids are among claimed polynucleotides of the convention that encode novel polypeptides, termed LBPs, capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed.
New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12619 BP; 3743 A; 2541 C; 2359 G; 3976 T; 0 other;
                                                                                                                                                                      Example 4; Fig 22; 143pp; English.
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Gaps ö

AAH26493 standard; DNA; 12619 BP.

RESULT 33 AAH26493 ID AAH26

2433 CCTTATGATCTGCCTGCCT 2451

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189 CCTTATGATCTGCCTGCCT 207

Law SW, Arjona AA;

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C195.1 protein; human PBWC cDNA library; cytokine activity; ss; peripheral blood mononuclear cell; nutritional activity; homology; cell proliferation/differentiation activity; EST; expressd sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poly:nucleotide(s) and proteins obtained from human PBMC, dendritic cell, adult brain, foetal brain and adult testes cDNA libraries used in research, detection and therapy of, e.g. cytokine and cell proliferation or differentiation
                                                       Nucleotide sequence of the 5' portion of the C195_1 protein.
                                                                                                                                                                                                                       /note= "no stop codon found at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                         Evans C, Jacobs K, LaVallie ER, Racie LA, Spaulding V, Treacy M;
                                                                                                                                                                                            /*tag= a
/product= "C195_1 protein"
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                         97WO-US10501
                              (first entry)
                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-063142/06.
P-PSDB; AAW42074.
                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                    WO9748801-A2
                                                                                                                                                                                                                                                                                                      16-JUN-1997;
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                              07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                         Bowman M, F
Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1998
                                                                                                                                                                                                                                                                              24-DEC-1997
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  AAV09268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                              Gaps
                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                   Drosophila melanogaster expressed polynucleotide SEQ ID NO 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 19; DB 23; Length 19175; Best Local Similarity 100.0%; Pred. No. 28; Matches 19; Conservative 0; Mismatches 0; Indels 0.
1.8%; Score 19; DB 22; Length 12619;
100.0%; Pred. No. 28;
Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19175 BP; 5148 A; 4250 C; 4561 G; 5216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 806; 21pp + Sequence Listing; English.
                            Indels
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                                                                                                                                                      ВР
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                                                                                                                                                   ABL02108 standard; cDNA; 19175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li PWD,
                                                                   Db 1940 CCTTTCCCAAATTCTACAA 1958
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                                                    CCTTTCCCAAATTCTACAA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609 GAGGCGGAGCCAGCTG 627
                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                        (first entry)
                            Conservative
                                                                                                                                                                                                                                                                           pharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /enter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
P-PSDB; ABB58005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY.
              Similarity
                                                                                                                                                                                                                                                                                                                                WO200171042-A2.
                                                                                                                                                                                                        26-MAR-2002
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 Query Match
                                                                                                                                                                            ABL02108;
                 Local
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AAV09268/c
ID AAV092
XX
              Best Loc
Matches
                                                    851
                                                                                                                        RESULT 34
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MCCOY JM;

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                                     This nucleotide sequence encodes the 5' portion of the C195_1 protein which was isolated from a human PBMC CDNA library. The products of the polynucleotides of the invention can be used in research, detection and therapy, as they may have nutritional activity, cytokine and cell prollferation/differentiation activity. A search against the Genbank database demonstrated that this sequence has at least some homology with two ESTs identified as "ygl1906.rl Homo sapiens CDNA clone 19937 5'" and "yml5f12.rl Homo sapiens CDNA clone 48025 5'".
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; C195_1; peripheral blood mononuclear cell; PBMC; protein factor; human; ds.
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                                                                                                                                                                                                                                                                             DB 19; Length 433; . 92;
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                                                                                                                                                                                                                                       Sequence 433 BP; 125 A; 85 C; 98 G; 125 T; 0 other;
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                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                             1.7%; Score 18;
100.0%; Pred. No.
ative 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
Claim 1; Page 47; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein C195_1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV04273 standard; cDNA; 433
                                                                                                                                                                                                                                                                                                                                                                   531 TGACATCATGTTCCAGCT 548
                                                                                                                                                                                                                                                                                                                                                                                                              341 IGACATCATGTTCCAGCT 324
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, memaropolesis regulating activity, issue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaenla; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemla, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 12534; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 22; Length 444;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 444 BP; 88 A; 110 C; 108 G; 138 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. w.
                                                               Human polynucleotide SEQ ID NO 12534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV86048/c
ID AAV86048 standard; cDNA; 451 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001; 2001WO-US04927
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                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-514838/56.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AA012543.
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                                                                                                                                                                                                                                                                             WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1999
                                                                                                                                                                                                                                 Homo sapiens
                   06-NOV-2001
                                                                                                                                                                                                                                                                                                                           07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV86048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA clone, designated C195_1, codes for a novel secreted protein (see AAW1600) of human peripheral blood monouclear cells (PBMC). It was isolated from a PBMC cDNA ilbrary using methods which are selective for cDNAs encoding secreted proteins. The 433 be sequence represents the 5' part of the clone; the 3' portion of C195_1, including the polyA tail, is provided in AAV04275. C195_1 is deposited as ATCC 98079, a composite clone. An additional isolate of C195_1, designated C195_4 (see AAV04274), is deposited as ATCC 98192. Both sequences can be recovered using a probe (see AAV04276). The isolated nucleic acid may be used to express recombinant secreted proteins; as a tissue/molecular weight marker; for chromosome clonefication; to identify possible genetic disorders; to isolate new related DNA; as a source of PCR primers; to generate anti-protein or anti-DNA antibodies; in interaction trap assays to identify sequences that encode interacting proteins etc. The secreted proteins can be used to screen compounds for biological activity; receptors and ligands and as nutritional sources. They may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   have biological activities, e.g. cytokine, cell proliferation or differentiation activity, immunosuppressant, immunostimulant, requiation of heamatopoiesis, modulation of fertility, chemotactic, chemokinetic, haemostatic, thrombolytic, antimicrobials, analgesic, antipsoriatic, etc. No evidence is given to support any of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding secreted protein from human peripheral blood mononuclear cells - useful, e.g. as immunomodulators, antitumour agents, promoters of tissue growth, haemostatic and thrombolytic agents etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA;
Spaulding V, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 433 BP; 125 A; 85 C; 98 G; 125 T; 0 other;
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100.0%; Pred. No.
                                                                 Location/Qualifiers
13..433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 35; 52pp; English.
                                                                                                                                                                                                                                                       97WO-US10500
                                                                                                                                                                                                                                                                                                                           96US-0664596
96US-0721926
                                                                                                                                                                                                                                                                                                     96US-0738367
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                                                                                                                  /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-063141/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW41600.
                        Homo sapiens
                                                                                                                                                             WO9748800-A1
                                                                                                                                                                                                                                                       16-JUN-1997;
                                                                                                                                                                                                                                                                                                                             17-JUN-1996;
27-SEP-1996;
                                                                                                                                                                                                                                                                                                     25-OCT-1996;
                                                                                         mat_peptide
                                                                                                                                                                                                              24 - DEC - 1997
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Gaps

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0; Indels

AAI92474 standard; cDNA; 444 BP.

RESULT 37 AAI92474

Query Match

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AA192474;

us-09-886-041-1.olig.rng

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2799; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 464 BP; 124 A; 105 C; 118 G; 117 T; 0 other;
                                                                                             Drmanac RT
                28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                          WPI; 2001-514838/56.
                                                              (HYSE-) HYSEQ INC.
                                                                                             Liu C,
                                                                                                                                          P-PSDB; AAO02808
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                                                                                                                                                                                                        disorders
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                                                                                           Tang YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, tissue given. Suggested activities haematopolesis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                               New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
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                                                                                                                                                                                                                     Lavallie ER, McCoy JM, Merberg D;
Treacy M;
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100.0%; Pred. No. 92;
ive 0; Mismatches 0; Indels
receptor; ligand; anti-inflammatory; tumour inhibitor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 451 BP; 128 A; 91 C; 102 G; 130 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 101; 633pp; English.
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                                                                                                                          98WO-US06954.
                                                                                                                                                       97US-0835913.
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                                                                                                                                                                                     (GEMY ) GENETICS INST INC
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                                                                                                                                                                                                                     J, Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                   WPI; 1999-070076/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                Homo saptens
                                                              WO9845435-A2
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                                                                                                                        10-APR-1998;
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                                                                                                                                                                                                                    Agostino MJ,
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                                                                                           15-0CT-1998
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AAI82739
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                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cardiovascular system antigen genomic DNA SEQ ID No 2262.
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DB 22; Length 464; 92;
                                                             0; Indels
                                   100.0%; Pred. No. 92; tive 0; Mismatches
   1.7%; Score 18;
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                                                                                                                                                               171 GCCCTGCACATAACCCT 188
                                                                                                                               791
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                                Local Similarity 100.
nes 18; Conservative
                                                                                                                               774 GGCCCTGCACATAACCCT
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00005-0179065 00005-0180628 00005-0180635 00005-0189874 00005-0190076 00005-0190076 00005-0205515 00005-021688 00005-021688 00005-021688 00005-021688 00005-021688	00005 0224518 000015 0224518 000015 0225214 000015 0225214 000015 022526 000015 0225270 000015 0225757 000015 0225757 000015 0225757 000015 022661 000015 022661 000015 022681 000015 022681 000015 022681 000015 022681 000015 022681	2000005 -023243 2000005 -023343 2000005 -0231243 2000005 -0231243 2000005 -0231244 2000005 -0231241 2000005 -0232081 2000005 -0232081 2000005 -0232397 2000005 -0232397 2000005 -023239 2000005 -0232400 2000005 -0232400 2000005 -0232400 2000005 -0232400 2000005 -0232400 2000005 -023364 2000005 -023423 2000005 -023423 2000005 -023423 2000005 -023423 200005 -0236365 200005 -0236365 200005 -0236365 200005 -0236365	0000S-0236370 0000S-0236802
1. JAN-2000; 4-FEB-2000; 2-A-FEB-2000; 6-MAR-2000; 7-MAR-2000; 9-MAR-2000; 9-MAR-2000; 7-JUN-2000; 9-MAR-2000; 7-JUN-2000; 1-J	4 ANG-2000; 4 ANG-2000; 4 ANG-2000; 4 ANG-2000; 4 ANG-2000; 4 ANG-2000; 4 ANG-2000; 5 ANG-2000; 5 ANG-2000; 7 ANG-2000; 7 ANG-2000; 7 ANG-2000; 8 ANG-2000; 8 ANG-2000; 9 ANG-2000; 1 SEP-2000; 1 SEP-2000; 1 SEP-2000; 1 SEP-2000;	SEP-2000;	9-SEP-2000; 2-OCT-2000;
P P R R R R R R R R R R R R R R R R R R	**************************************		R. R.

2000US-0237040 2000US-0237040 2000US-0240937 2000US-02411785 2000US-02411809 2000US-02411809 2000US-02411809 2000US-02411809 2000US-0246474 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246521 2000US-0249209 2000US-0249209 2000US-0249201 2000US-0251030 2000US-0251030 2000US-0251089 02-0CT-2000)
02-0CT-2000)
03-0CT-2000)
03-0C 3

SX X Ruben (HUMA-) HUMAN GENOME SCI INC

Barash SC, Rosen CA,

New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -WPI; 2001-451930/48.

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14-AUG-2000;
18-AUG-2000;
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08-SEP-2000;
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22-AUG-2000;
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  Sequences AAS35741-AAS36842 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention.

Cardiovascular system antigens and their associated polynocleotides are cardiovascular system antigens and their associated polynocleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmne system antigen polynucleotide. The treatable disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, viruses and fungi, ocular disorders such as correal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glence to pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotrasis.

Cransplantation, but was obtained in electronic format directly from WIPPO correct transplantation, but was obtained in electronic format directly from WIPPO correct are from the properties of the prevent served are for this patent did not form part of the printed at free figures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chicken; sheep; immunosuppressive; antiarthritic; vascropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; immicrofective; corpthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; descebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; reapliascroprisconding disorder; wound healing; skin aging; organ transplantation; tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cardiovascular system antigen genomic DNA SEQ ID No 2263.
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                                                                                                                                                                                                                                                                                                                                                                                  1.7%; Score 18; DB 22; Length 477;
100.0%; Pred. No. 92;
tive 0; Mismatches 0; Indels
           Claim 1; SEQ ID No 2262; 674pp; English.
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2000US-018464.
2000US-0186350.
2000US-0189874.
2000US-0198076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ACCCAAGCAGCCAGGACA 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                         894 ACCCAAGCAGCCAGGACA 911
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17-MAR-2000;
18-APR-2000;
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02-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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chickens or sheep. A pathological condition can be determined by chickens or sheep. A pathological condition can be determined by effecting the presence or absence of a mutation in a cardiovascular system antigen polymuclectide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neotharsms of the breast or liver, cardiovascular disorders such as cardiovascular disorders such as cardiac arrest, cardencesular disorders such as cardiac arrest, cardencesular disorders such as cerebral ischmemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruseg and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as premature labour and infertility, as glomerulonephrifis and respiratory disorders such as sathma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotraxis.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/published_pot_sequences.
                                                                                                                                                                                                                                                                                                            1.7%; Score 18; DB 22; Length 477; 100.0%; Pred. No. 92; tive 0; Mismatches 0; Indels
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hyperproliferative de
cerebrovascular diso
fungal infection; Vi
gastrointestinal dis;
wound healing; skin
anti-infertility.
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Best Local Similarity
Matches 18; Conserv
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24-FEB-2000;
02-MAR-2000;
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17-MAR-2000;
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polypucleotides are useful in the diagnosis, treatment and prevention of various types of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -
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                                                  2000US-0241787.
2000US-0241808.
2000US-0241809.
2000US-0241826.
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08 - NOV - 2000)
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06-DEC-2000;
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05-DEC-2000;
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05-JAN-2001;
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17-NOV-2000;
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Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autolimune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ss; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; wound healing; skin aging; organ transplantation; tissue regeneration;
                                                                                Human cardiovascular system antigen cDNA polynucleotide SEQ ID No 526
CDNA; 489 BP.
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07-JUL-2000;
11-JUL-2000;
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2000US-0218290.
2000US-0220963.
2000US-0220964.
2000US-0224518.
2000US-0224518.
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2000US-0225747.
2000US-0225759.
2000US-0225759.
2000US-0226279.
2000US-022688.
2000US-022688.
2000US-022888.
2000US-0228924.
2000US-02289343.
2000US-0229344.
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2000US-0236367.
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111-JUL-2000, 25-4-JUL-2000, 26-JUL-2000, 26
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20000S-024652 20000S-0246525 20000S-0246526 20000S-0246528 20000S-0246528 20000S-0246609 20000S-0246610 20000S-0246611 20000S-0246611 20000S-0246611 200005-0249210 200005-0249211 200005-0249212 200005-0249213 200005-0249214 2000US-0246474. 2000US-0246475. 2000US-0246476. 2000US-0246477. 2000US-0246477. 2000US-0249244. 2000US-0249245. 2000US-0249264. 2000US-0249297. 2000US-0249297. 2000US-0249297. 2000US-0250160 2000US-0250180 2000US-0251988 2000US-0251988 2000US-025185 2000US-0251858 2000US-0251868 2000US-0251868 2000US-0249216. 2000US-0249217. 2000US-0249218. 2000US-0249208 2000US-0249209 2000US-0254097 2001US-0259678 01-NOV-2000; 08-NOV-2000; 08-NO 17-NOV-2000; 217-NOV-2000; 217 17-NOV-2000; 7-NOV-2000; 01-DEC-2000; 01-DEC-2000; 06-DEC-2000; 08-DEC-2000; 05-JAN-2001; 

Ruben SM (HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC,

WPI; 2001-451930/48. P-PSDB; AAU22367.

New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -

Claim 1; SEQ ID No 526; 674pp; English.

Sequences AAS35126-AAS35740 represent cDNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as

an additional isolate of clone C195\_1 (see AAV04273), deposited

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             nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate itssues and in chemotaxis.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA clone, designated C195_4, codes for a novel secreted protein (see AAW41601) of human peripheral blood mononuclear cells (PBMC). It was isolated from a PBMC cDNA library using methods which are selective for cDNAs encoding secreted proteins. The 733 bps sequence represents the internal part of the clone; the 3' portion of C195_4, including the polyA tail, is provided in AAV04278, and the 5' portion in AAV04277. C195_4 is deposited as ATCC 98192.
cerebrovascular disorders such as cerebral ischaemia,
                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                 22; Length 489;
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92;
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                                                                                                                                                                                                                   Score 18;
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13..733
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96US-0664596.
96US-0721926.
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 cardiac arrest,
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17-JUN-1996;
27-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
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              ARAV04776. The isolated clone acid may be used to express recombinant secreted proteins; as a tissue/molecular weight marker; for chromosome identification; to identify possible genetic disorders; to isolate related DNA; as a source of PCR primers; to generate anti-protein or anti-DNA antibodies; in interaction trap assays to identify sequences that encode interacting proteins etc. The secreted proteins can be used to screen compounds for biological activity; to raise antibodies; as tissue markers; for isolation of related receptors and ligands and as nutritional sources. They may
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                              related receptors and ligands and as nutritional sources. They may also have biological activities, e.g. cytokine, cell proliferation or differentiation activity, immunosuppressnt, immunostimulant, regulation of haematopolesis, modulation of fertility, chemotactic, chemokinetic, haemostatic, thrombolytic, antimicrobials, analgesic, antipsoriatic, etc. No evidence is given to support any of these
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100.0%; Pred. No. 92;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 TGACATCATGTTCCAGCT 324
                                                                                                                                                                                                                                                                                                                       activities or applications.
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Best Local Similarity 100.
Matches 18; Conservative
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414

Erepresent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAA825620 to AA825650 represent Potestate DNA sequences; AAA81321 represent Potestate DNA sequences; AAA81324 to AAA81322 and AAA81321 represent Potestate DNA sequences; and AAA81322 to AAA81452 and AAA81321 represent DNA sequences; and AAA81322 to Sequences, which are all used in the exemplification of the present to invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition of the nucleic acid sequences, protein sequences, and antibodies of medicament) for treating preventing or diagnosing infection due to Neisserlal bacteria. For example, some of the identification of sequences and/or against all pathogenic Neissariae. Identification of sequences and/or against all pathogenic Neissariae. Identification of sequences and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, CC Particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have also been tried but none have successfully covercome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
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Ratti G, Scarselli M, Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
                                                Gaps
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  1.7%; Score 18; DB 22; Length 757;
100.0%; Pred. No. 92;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  N. meningitidis partial DNA sequence gnm_139 SEQ ID NO:139.
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C, Mora M,
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ID AAA81592 standard; DNA; 767 BP.
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99US-0132068
                                                                                                              350 GCATCATCTTATTTGCT 367
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Query Match 1.7
Best Local Similarity 100.
Matches 18; Conservative
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Masignani V, Galeotti
Rappuoli R, Pizza M;
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                                                            DB 21; Length 767;
                             Sequence 767 BP; 215 A; 144 C; 155 G; 253 T; 0 other;
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                                                                         100.0%; Pred. No. 92; tive 0; Mismatches
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Job time : 247 secs
                                                          1.7%; Score 18;
other more variable regions.
                                                                                                                        912 CTCAAAACACAAAGGCC 929
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                                                                       Best Local Similarity 100.0
Matches 18; Conservative
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AX148182 Sequence
AX299705 Sequence
AX338373 Sequence
AX305131 Sequence
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AX205131 Homo sapi
AX33834 Sequence
AX277635 Sequence
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AX14791 Sequence
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1041)

Vogell,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,

Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,

Sejlitz,T. and Muff,R.M.

Novel g protein-coupled receptors

Patent: WO 0136473-A 79 25-MAY-2001;

PHARMACIA & UPJOHN COMPANY (US)
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AX147834
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/organism="Homo sapiens"
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che r	ocal Similarity 100.0%; Fred. No. s 1041; Conservative 0; Mismatch	1021 CACATTGTTGAGTGGCACTGA
	1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG 60	 AX148182 AX148182
e e	61 CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCATGGGGTCGCCCTGTGTGGTTTC 120	 Sequence 23 110m Facent Woolson AX148182 AX148182.1 GI:14347084
121 121	1 IGCTICCACATGAAGACCTGGAAGCCCAGCACTGTTTACATTTGGCCGTGGCT 180	SOURCE Auman. ORGANISM HOmo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
181 181	1 GATTICCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240 	
241	1 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC 300	 maceuticals ocation/Qua
301	1 GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC 360	 Appension of the property of
361 361	1 CACCACGGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG 420	Query Match 100.0%; Score 1041; DB 6; Length 1041; Best Local Similarity 100.0%; Pred. No. 0; Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
421	21 GCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG 480 	Oy 1 ATGTACAACGGGTCGTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG 60
481	1 ACGCCGTCTCCTGTGAGAGCTTCATCATGGAGTCGGCCAATGGCTGGC	 QY         61         CTGCTCATTGTGGCCTTTGTGCTGGCGCACTAGGCATGGGGTCGCCCTGTGTGGTTTC         120           Db         61         CTGCTCATTGTGGCCTTTGTGGCGCCACTAGGCAATGGGGTCGCCCTGTGTGTTTC         120
541 541	1 TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT 600	 OY 121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTACCTTTTCAATTTGCCCGTGGCT 180
601 601	1 TGGAGCCTGAGGCGGAGGCAGCAGCTGGCCAGACACGGCTCGGATGAAGAAGGCGACCCGG 660 	Qy 181 GATITCCTCCTIATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
661 661	1 TTCATCATGGTGGCGCAATTGTGTTCATCACGTGCTGCCTGC	 OY 241 TGGGCTTTTGGGGACATTCCCTGCGGGTGTGTTCACGTTGGCCATGAACAGGGCC 300 241 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC 300
721	1 CTCTATITCCTCTGGACGGTGCCCTCGATGCCTGCGATCCCTCTGTCCATGGGCCCCTG 780	 Qy 301 GGGAGCATCGTGTTCCTTACGGTGGTGCTGCGGACAGGTATTTCAAAGTGGTCCACCC 360 
781 781	81 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT 840	QY         361         CACCAGGGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCTGTGG         420           1         2
841 841	1 TCAAGCCCTCCTTTCCCAAATTCTACAACAGCTCAAAATCTGCAGTCTGAAACCCAAG 900 	QY 421 GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAACCATCTCTGCGTGCAAGA 480
9 9	01       CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGATGCCAATTTCGAACCTCGGTCGC       960         11	 QY 481 ACGCCCGTCTCCTGTGAGCTTCATCATGGAGTCGCCCATGGCTCGCTGATGACATCATG 540
96	61 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020 	QY 541 TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTGCTCCTTCAAGATTGTT 600 111111111111111111111111111111111

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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          CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
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                                     TICATCATGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
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Ye,J.C., Cravchik,A.C., di Francesco,V.C. and Beasley,E.M Isolated human g-protein coupled receptors, nucleic acid encoding human aper proteins, and uses thereof Patent: WO 0173029-A 1 04-OCT-2001;
PE Corporation (NY) (US)
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Homo sapiens G protein-coupled receptor (GPR81) gene, complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Majumder,K., Vernet,C.A., Casman,S.J., Wolenc,A.R., Spaderna,S.K.,
Padigaru,M., Mishnu,V.S., Tchernev,V.T., Spytek,K.A., Li,L.,
Baumgartner,J.C. and Gusev,V.Y.
Novel proteins and nucleic acids encoding same
Patent: WO 0174904-A 1 11-OCT-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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S Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vanti,W.B., Arkhitko,O., Lew,D.K., Nguyen,T., Cynch,K.R., Cheng,R., Vanti,W.B., Arkhitko,O., Lewis.T., Evans,J.F., George,S.R. and O'Dowd,B.F.
Direct Submission
Losting (17-Aug-2001) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada Location/Qualifiers
Location/Qualifiers
1. 1041
| John Sapiens Homo sapiens | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Corp. Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Location/Qualifiers | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Corp. Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada | Addle Creek Rd. Rm. 4353, Toronto, O
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/translation="MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHM
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TANSCESFINESANGWHDINFOLEFERPLGIILECSFKTVWSLRRRQQLARQARMKKA
TRFIMVVAIVFITCYLDSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPL
l (bases 1 to 1041)
Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O.,
Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
Discovery and mapping of ten novel G protein-coupled receptor genes
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Location/Qualifiers
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llarity 100.0%; Pred. No. 0;
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/db_xref="taxon:9606"
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Db 223 GATTTCCTCCT	Qy 241 TGGGCTTTTGG	Oy 301 GGGAGCATCGT 	361	Oy 421 GCCTGGTCAT 	Qy 481 AGGCCGTCTC	Qy 541 TTCCAGCTGGA 	Qy 601 TGGAGCCTGAG 	Oy 661 TTCATCATGGT              Db 703 TTCATCATGGT	Qy 721 CTCTATTCCT              Db 763 CTCTATTCCT	Oy 781 CACATAACCCT 	Oy 841 TCAAGCCCTC 	Oy 901 CAGCCAGGACA 	Qy 961 AGGAGTTCCAT             Db 1003 AGGAGTTCCAT	Oy 1021 CACATTGTTGA 	RESULT 8 AX277635 LOCUS AX277635	ACCESSION AX277635 VERSION AX277635 KEYWORDS Numan	Mag W	REFERENCE 1 (sites   AUTHORS Xiao,Y.
661 TTCATCATGGTGGTGGCAATTGTGTTCACATGCTACCTGCCCAGCGTGTCTGCTAGA	Db 666 TTCATCATGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA 725  Qy 721 CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG 780	Db 726 CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG 785 Qy 781 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCTGGTGTATTATTT 840		OY 901 CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC 960	Oy 961 AGGAGTIGCAICAGIGIGGAAATAGITICCAAAGCCAGTCIGAIGGCAAIGGGATCCC 1020 	1021 CACATTGTTGAGTGCACTGA 1041    -		AX305131 AX305131 1083 bp DNA linear PAT 11-DEC-2001 DEFINITION Sequence 11 from Patent W00187937.  AX305131 AX305131 CT:17544756		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (sites) AUTHORS Patterson,C., Lu,DA, Thornton,M., Triboullay,C.M.,	Useduria, Annalia, A., Gedunia, A., Walle, N., Nguyen, D., S., Ine, H., Hafalla, A., Elliott, V.S., Lal, P., Reddy, R., Kallick, D.A., Tang, T.Y. and Au-Young, J. TITLE G-protein coupled receptors.	Incyte Ge	/organism="Homo sapiens" //db_xref="taxon:9606" //db_xref="incyte 10 No: 7474846CB1"   Ancte="Incyte 10 No: 7474846CB1"   Ancte="Incyte 10 September 20 Count 10 September 20 Co	Ortoin Query Match 100.0%; Score 1041; DB 6; Length 1083; Best Local Similarity 100.0%; Pred. No. 0; Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy     1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGACACCATCTCCCAGGTGATGCCGCCG     60       LILILILILILILILILILILILILILILILILILILI	Qy     61 CTGCTCAT#GIGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120       111111111111111111111111111111111111	Qy 121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180	Qy 181 GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACGACTATTACCTCAGACGTAGACAC 240

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Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                     Ye,J.C., Cravchik,A.C., di Francesco,V.C. and Beasley,E.M. Isolated human g-protein coupled receptors, nucleic acid encoding human gpcr proteins, and uses thereof Patent: WO 0173029-A 3 04-OCT-2001; PE Corporation (NY) (US)
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Regulation of human hm74-like g protein
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Carlaria; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 179172)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrocks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Blimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bunay, C., Benton, J., Burage, K., Brown, M., Bryant, N.P., Buhay, C., Burcell, K. L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Dapper, H., David, R., David, R., David, M.L., Draper, H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Esochto, M., Falls, T., Ferraquico, D., Flaggin, M., Ford, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homasl, F., Howard, S., Huber, J., Hully, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
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                      TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
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                                                                                   TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
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AC026331.18 GI:14547388
HTG; HTGS_PHASEL; HTGS_DRAFT; HTGS_FULLTOP.
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Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, L., Li, L., Licker, E., Lidu, C., Liu, M.,
Loulseged, H., Lozado, R.J., Lu, X., Lucter, A., Lucter, R., Luna, R.,
Martinez, E., Massey, E., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mached, P., Maedor, M.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, N.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, N.,
Mouyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
Oqui, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, M., Nolaboar, I., Rolfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, R.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
Wallington, S., Williams, G., Williamson, A., Walczyk, R., Wooden, S.,
Wallington, S., Williams, G., Williamson, A., Walczyk, R., Wooden, S.,
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Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 31% of reads
Chemistry: Dye-primer Bodipy: 31% of reads
Chemistry: Dye-terminator B19 Dye: 69% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 17881 bases at least Q40
Consensus quality: 17865 bases at least Q30
Consensus quality: 179678 bases at least Q20
Estimated insert size: 176741; sum-of-contigs estimation
Quality coverage: 9.4x in Q20 bases; sum-of-contigs estimation
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Center: Baylor College of Medicine Center: Baylor College of Medicine Meb site: http://www.hgsc.bcm.tmc.edu/Contact: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.
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Center clone name: RPI1-507N20
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Worley, K.C.
Direct Submission
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1078 167351: contig of 6274 bp in length 1352 167451: gap of unknown length 1352 173489: contig of 5938 bp in length 1390 173489: gap of unknown length 1490 17658: contig of 2769 bp in length 1359 176518: gap of unknown length 1359 176518: contig of 2764 bp in length 15678: contig of 2764 bp in length 15678 176712: contig of 2814 bp in length.
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                                                                                                                                                                       /clone="RP11-507N20"
a 39904 c 41184 g 47913
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/db_xref="taxon:9606"
                                                                                                                                                             /chromosome="12"
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                                                             1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG
                                                                                                                                                                                                                                                        GATTICCTCCTTATGATCTGCCTGCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
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Sequencing vector: Plasmid; M7789
Sequencing vector: M3; L08821
Chemistry: Dye-primer Bodipy: 8% of reads
Chemistry: Dye-terminator Big Dye: 92% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 208507 bases at least Q40
Consensus quality: 208562 bases at least Q30
Consensus quality: 210152 bases at least Q30
Estimated insert Size: 205209; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                               Worley, K.C.
Direct Submission
Submitted (22-MAR-2000) Human Genome Sequencing Center, Department
                                                                          of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 30, 2001 this sequence version replaced g1:14861654.
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50546: gap of unknown length
93563: contig of 43017 bp in length
93663: gap of unknown length
122547: contig of 28884 bp in length
140900: contig of 18253 bp in length
140000: contig of 18253 bp in length
152275: contig of 11275 bp in length
153275: gap of unknown length
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                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                            Center: Baylor College of Medicine Center code: BCM
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/db_xref="taxon:9606"
/chromosome="12"
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Center clone name: RP11-324E6
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 888)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 11 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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                                                        CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
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Sequence 11 from Patent WO0136473.
AX147766
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/db_xref="taxon:9606"
a 254 c 231 g 229
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llarity 100.0%; Pred. No. (
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adjunder, K., Vernet, C.A., Casman, S.J., Wolenc, A.R., Spaderna, S.K.,
Padigaru, M., Mishuu, V.S., Tchernev, V.T., Spytek, K.A., Li, L.,
Baumgartner, J.C. and Gusev, V.Y.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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99.8%; Pred. No. 0;
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/db_xref-"taxon:9606"
318 c 295 g 275
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Sequence 4 from Patent W00174904
AX338374
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AX338374.1 GI:18128871
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bass 1 to 1092)
Chen.R., Dang, H.T. and Lowitz, K.P.
Endogenous and non-endogenous versions of human g protein-coupled
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AXX48194
AXI48194.1 GI:14347090
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/db_xref="taxon:9606"
320 c 273 g 271
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Young/P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nomura, H., Nielsen, B.W. and Matsushima, K.
Moncaular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide receptors
Int. Immunol. 5 (10), 1239-1249 (1993)
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llarity 100.0%; Pred. No. 1.6e-05;
Conservative 0; Mismatches 0;
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        Score 32; DB 6; L
Pred. No. 1.7e-05;
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patent: WO 0194629-A 6104 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualiflers
3.1%; scc. 100.0%; Pred. No. ... 0; Mismatches
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Sequence 6104 from Patent WO0194629.
AX335595
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/db_xref="taxon:9606"
530 c 525 g 520
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0762-60-7704.
Location/Qualifiers
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Cancer Res. Inst., Kani
13-1 Takaramachi
Kanazawa, Ishikawa 920
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Human mRNA for HM74.
D10923
D10923.1 GI:219866
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Gaps

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PAT 08-JUN-2001
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artificial sequence.

1 (bases 1 to 24)

Vogeli, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P., Slightom, J., Schellin, K.A., Raytes, P.S., Bannigan, C.M., Ruff, V., Sejlitz, T. and Huff, R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 162 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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artificial sequence.

I (bases 1 to 52.)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Raytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 130 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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1 (bases 1 to 52)
Sughtlon, Wood, L. S., Parodi, L. A., Hiebsch, R. R., Lind, P.,
Slightom, J., Schelllin, K. A., Kaytes, P. S., Bannigan, C. M., Ruff, V.,
Sejlitz, T. and Huff, R. M.
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Sequence 159 from Patent WO0136473.
AX147914
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Sequence 130 from Patent WO0136473.
AX147885
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    /organism="synthetic cc/db_xref="taxon:32630"
    /note="Novel Sequence"

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/db_xref="taxon:32630"
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/Product="HA74"
/Product="HA74"
/Protein_id="BAA01721.1"
/db_xref="G1:219867"
/dc_xref="G1:219867"
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Vogell, G., Wood, L.S., Parodl, L.A., Hiebsch, R.R., Lind, P.,
Slightom, J., Schellin, K.A., Kaytes, P.S., Bannigan, C.M., Ruff, V.,
Sejlitz, T. and Huff, R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 133 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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100.0%; Pred. No. 1.6e-05;
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/db_xrsf="taxon:32630"
/note="Novel Sequence"
/ c 5 9 t
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100.0%; Pred. No. 0.66;
tive 0; Mismatches
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/db_xref="taxon:9606"
/cell_line="human monocyte"
/cell_type="monocyte"
61. .1224
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AX147917.1 GI:14346912
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Sequence 133 from Patent W00136473.
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/codon_start=1
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RESULT 17 AX147888 LOCUS

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AJ300199.1 GI:11558405
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/codon_start=1
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59. .1141
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Pfeffer, K.
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Watches 23; Conservative
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Schaub, A., Futterer, A. and Pfeffer, K.
PUMA-G, an interferon-gamma inducible gene in macrophages is a novel member of the seven transmembrane spanning superfamily Unpublished
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Vodeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,

Slightcm,J. Schellin,R.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,

Sejlitz,T. and Huff,R.M.

Sejlitz,T. and Huff,R.M.

Povel g protein-coupled receptors

Patent: WO 0136473-A 108 25-MAY-2001;

PHARMACIA & UPJOHN COMPANY (US)
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/db_xref="taxon:32630"
/note="Novel Sequence"
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                                                                        /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Novel Sequence"
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100.0%; Pred. No. 2.1;
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100.0%; Pred. No. 0.58;
 Novel g protein-coupled receptors
Patent: WO 0136473-A 159 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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Pfeffer, K.
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/translation="MSSSDHFLVINGKNCCVFRDENIAKVLPPVLGLEFVFGLLGNGL
ALWIFCFHLKSWKSSRIFLFNLAVADFLLITCLPFFLTDNYVHNWWRFGGIPCRVMLF
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YTHMYTKRANGAYLCSSFFICTVFRWHDAMFLLEFFLPLAIILFCSGRIWSRCRMD
RHAKIKRANGALVATVFICFLPSVAVRIRIEWLLYKYNVRNCDIYSSVDLAFFTI
LSFTYMNSMLDPVVYYFSSFSFPPFFSTCINRCLRKKTLGEPDNNRSTSVELTGDPST
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/protein_id="CAC17790.1"
/db_xref="GI:11558404"
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Mus musculus Puma-g gene for putative seven transmembrane spanning
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Schaub,A., Futterer,A. and Pfeffer,K. PUMA-G, an interferon-gamma inducible gene in macrophages is a novel member of the seven transmembrane spanning superfamily
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Submitted (10-NOV-2000) Pfeffer K., Institute of Medical
Microbiology, Immunology and Hygiene, Technical University of
Munich, Trogerstr. 9, Munich, D-81675, GERWANY
Location/Qualifiers
1. 7100
Direct Submission Submitted (10-NOV-2000) Pfeffer K., Institute of Medical Submitted (10-NOV-2000) Pfeffer K., Institute of Medical Microbiology, Immunology and Hygiene, Technical University of Munich, Trogerstr. 9, Munich, D-81675, GERMANY Location/Qualifiers
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/cell_line="ANA-1"
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/gene="Puma-g"
1909. .1914
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Further information can be found at
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ALWIFCFHLKSWKSSRIFLFRLAVADFLLICLPFTDNYVHWDWRFGGIPCRYMLF
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3545. 4323
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4211. 4216
/gene="Puma-g"
4211. 4216
/gene="Puma-g"
1670 g 1890 t
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Human DNA sequence from clone RP11-569E4 on chromosome 13, complete
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                                                                                                                       /product="putative seven transmembrane spanning receptor"
/protein_id="CAC17791.1"
/db_xref="GI:11558406"
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Mashreghi-Mohammadi,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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cell, BAC clone"
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'note-"129/SVJ ES
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2404. 417
                                       /gene="Puma-g"
/2462. 35.4
                                                                            2462. .3544
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AL390918
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JOURNAL
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AL390918
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                                                                           CDS
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http://www.sanger.ac.uk/HGDP/Chri3
RP11-569E4 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/Dacpac/home.htm
VECTOR: pBAACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-569E4 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-322A14 is at 83451 in this sequence. The true right end of clone RP11-141M24 is at 100 in this
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/1428. 7475
/note="12 copies 4 mer gtgt 95% conserved"
8238. .8535
/note="Aligo repeat: matches 1. .309 of consensus"
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/note="match: GSS: Em:AQ052321 Em:AQ386521"
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/note="2 copies 28 mer 96% conserved"
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/note="match: GSS: Em:AQ560705"
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complement(14350. 14638)
/note="match: GSS: Em:B89417"
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1341. .1626
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complement(1. .88)
/note="match: GSS: Em:AQ38
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// Anote-"L2 repeat: matches 1796. .2267 of consensus"
35152. .35237
                                                                              /note="Alusx repeat: matches 1. .312 of consensus"
1857. .1905.
/note="match: GSS: Em:AQ322687"
/note="LIM4 repeat: matches 4074. .4207 of consensus note="LIM4 repeat: matches 4074. .4207 of consensus note="LIM5 copies 2 mer ac 100% conserved"
20391. .20695
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/note="80 copies 2 mer tc 68% conserved"
29563. 29844
/note="Aluga repeat: matches 1. 282 of consensus"
30820. 30988
/note="MIR repeat: matches 17. 193 of consensus"
/note="MIR repeat: matches 57. 261 of consensus"
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                               .198 of consensus"
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complement(19901. 40653)
/note="match: GSs: Em:A6541398"
complement(40197. 40653)
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complement(37055, .37577)
/note="match: GSS: Em:AQ670939"
38649, .38857
                         note="MIR repeat: matches 36. 7778. 18088
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases; I to 1256,4)

MuznyD, M., Admas,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Bustbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Burbaria,J., Burket,C., Burrell,K.L., Byrd,M.C., Carron,T.F., Carron, T.F., Carron, Dathorne,S.R., David,R.L., Dauck,J., Dauck,J., Dathorne,S.R., David,R.L., Garcia,A., Garcia,A., Garcia,A., Garcia,A., Garcia,A., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hennadez,J., Hernandez,J., Hensid,R.L., Jak,Y., Johnson,R., Jolnson,R., Marish,R., Marsin,R., Maneshwari,M., Maneshwari,M., Maner,G., Martin,R., Martin,R., Martindale,A., Martinez,E., Maxer,M., Maner,G., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martindale,A., Martin,R., Martin,R.,
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Homo sapiens chromosome 12 clone RP11-290121, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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AC012158.30 GI:17402749
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                     40677, .40951
/note="match: GSS: Em:AQ543863"
complement(41575, .41939)
/note="match: GSS: Em:AQ349212"
                                                                                                                                                     complement(41575. .41939)
/note="match: GSS: Em:AQ100514"
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AC012158/c
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KEYWORDS
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AC011080.3 GI:11024919
HTG; HTGS_PHASE2; HTGS_DRAFT.
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                                                                                  ORGANISM
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AUTHORS
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             VERSION
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                                                             SOURCE
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NOTE: This is a "working draft' sequence It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                Submitted (21-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Dec 7, 2001 this sequence version replaced gi:17155006.

Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-primer Bodipy: 2% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155117 bases at least Q40
Consensus quality: 155780 bases at least Q30
Consensus quality: 155780 bases; almacion
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 8.8x in Q20 bases; sum-of-contigs estimation
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmanl, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 1.7;
tive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Contact: project Information
Center project name: HNQA
Center clone name: RP11-290121
Sequencing vector: Plasmid; N7789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-290121"
44420 a 31059 c 31169 g 45911 t
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/db_xref="taxon:9606"
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                                                                                                                                                                                                           Worley, K.C.
Direct Submission
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Best Local Similarity
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                                                                                                                                                                                                                                           AUTHORS
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Balewin, J., Barna, N., Beckerly, R., Bogulalarkiy, L., Boukhaler, B.,

Balewin, J., Barna, N., Calangelo, M., Collins, S., Collymore, A.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Ferrelia, P., Fitzlugh, M., Forrest, C., Funke, R., Gage, D.,

Ferrelia, P., Fitzlugh, M., Forrest, C., Funke, R., Gage, D.,

Ferrelia, P., Fitzlugh, M., Forrest, C., Funke, R., Gage, D.,

Howland, J. C., Lidua, C., Locke, K., Macdonald, P., Marquis, N.,

McDean, J. Cardyna, S., Gran, C., Mann, L., Karatas, A., Klein, J.,

McDean, J. Cardyna, S., Gran, C., Mann, L., Karatas, A., Klein, J.,

McDean, J. C., Lidua, C., Locke, K., Macdonald, P., Marquis, N.,

McDean, J. Naylor, J., Norman, C. H., O'Connon, T., O'Doneall, P.,

McDean, J., Naylor, J., Norman, C. H., O'Connon, T., O'Doneall, P.,

Restardo, J., Ve, W., J., Zimmer, A. and Zody, M.

Direct Submission

No. Ye, W., J., Zimmer, A. and Zody, M. O'A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W., J., Zimmer, A. and Zody, M. O'A., Wheeler, J., Wu, X.,

Myman, J., Zoharles Street, Cambridge, M. O'A., Wheeler, J., Wu, X.,

Myman, J., Zoharles Street, Cambridge, M. O'A., Wheeler, J., Wu, X.,

Myman, J. St. Charles Street, Cambridge, M. O'A., Wheeler, J., Wu, X.,

Myman, J. So'Dharles Street, Cambridge, M. O'A., Wheeler, J., Wu, X.,

Myman, J. So'Dharles Street, Cambridge, M. O'A., Wheeler, J., Wu, X.,

Myman, J. So'Dharles Street, Cambridge, M. O'A., Wille, C.

Center, Submission

Mity: A. Green, P. (1966-1997)

Http://fyle.genome.washington.edu/RW/Repeatwasker.html

Contest: sequence_submissions@genome.wi.mit.edu

Contest: Mitchelad Institute/MYMW-seq.wi.mit.edu

Contest: Mitchelad Institute/Mymw-seq.wi.mit.edu

Contest: Submisty: Packers in Phacy vector: Mis. Willy Mys. 100% of reads

Sequencing vector: Nis. Willy Mys. 100% of reads

Sequencing vector: Nis. Willy Mys. 100% o
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183735)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-45K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             provided by the submitters.
This sequence will be replaced
by the finished sequence as soon as it is available and
the finished sequence as soon as it is available and
the accession number will be preserved.
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21444 183735: contig of 162292 bp in length.
Location/Qualifiers
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/note="assembly_fragment
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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AUTHORS
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Manmallia Eucherlai, Primates; Catarrinn; Hominidae; Homo.

Murny, D.M., Adams, C., Adio-Oddola, P., Ali-Osman, F.X., Allen, C.,

Murny, D.M., Adams, C., Adio-Oddola, S., Alvele, M., Banks, T.,

Barbardoks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

Bundy, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,

Carron, T.F., Carter, M., Cavazos, S.R., Chackon, M., Enyad, N.C.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Chen, G., Chen, R., Draper, H., Dugar, Rocha, S.R., David, R.,

Dealaney, K.R., Draper, H., Dugar, Rocha, S., Durbin, K.J.,

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

Earnhart, C., Edgar, M., Gunarane, P., Hale, S., Hamilton, K.,

Earnhart, C., Edgar, M., Gunarane, P., Hale, S., Hamilton, K.,

Earnhart, C., Edgar, M., Gunarane, P., Hale, S., Hamilton, K.,

Gorrell, J.H., Guevara, W., Gunarathe, P., Hawes, A., Harnandez, O., Hoddson, A., Hogues, M., Holloway, C., Hollins, B.,

Herrandez, O., Hoddson, A., Hogues, M., Holloway, C., Hollins, B.,

Herrandez, O., Hoddson, A., Hogues, M., Holloway, C., Hollins, B.,

Herrandez, O., Hoddson, A., Hogues, M., Holloway, C., Howlins, B.,

Marisson, E., Kally, S., Chan, U., King, L., Korvah, J., Kovar, C.,

Kratovic, J., Kureshi, A., Luoier, R., Luna, R., Ma, J.,

Mansey, E., Hawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,

Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,

Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Nauts, S., Savery, G.,

Scodergrane, R., Soott, G., Shen, H., Shooshtati, N., Sison, I.,

Sulerer, S., Scott, G., Warten, R., Washington, C., Wallianson, A., Syatek, A., Tamerisa, R., Wang, S., Wall, K., Wang, Y. E.,

Sulerer, S., Wall, Y. Wu, Y. Wu, Y. W., Shou, J., Sooter, S., Wall, S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC055724 1199607 bp DNA linear HTG 31-JAN-2002 Homo sapiens chromosome 12 clone RP11-985023, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                      Length 183735;
                                                                                                                                                  104 others
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1.6;
                                                                                                                   vector_side:right"
56460 a 33977 c 35374 g 57820 t
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                        21444. 183735
/note="assembly_fragment
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HTG; HTGS_PHASE1.
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                                                                                   clone_end:T7
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Best Local Similarity 100.
Matches 22; Conservative
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                               misc_feature
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AC055724/C
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AUTHORS
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KEYWORDS
SOURCE
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(bases 1 to 199607)

REFERENCE

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft" sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Worley, K.C.
Direct Submission
Submitted (18-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jan 31, 2002 this sequence version replaced gi:10086369.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 173746 bases at least Q40
Consensus quality: 186262 bases at least Q30
Consensus quality: 192992 bases at least Q20
Estimated insert size: 196552; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarcose-fp estimation
Quality coverage: 2.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-primer Bodipy: 50% of reads
Chemistry: Dye-terminator Big Dye: 50% of reads
Assembly program: Phrap; version 0.990329First call to
findPhraphist
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18144: gap of unknown length
36046: contig of 17902 bp in length
36142 contig of 17578 bp in length
48724: contig of 12578 bp in length
48824: gap of unknown length
58725: contig of 9901 bp in length
58825: gap of unknown length
70015: contig of 11190 bp in length
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of 13699 bp in length
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of 11475 bp in length
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of 8918 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Center clone name: RP11-985023
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IEAVTANSFINATHLKEINLSHNKTKSQKIDYGVFAKLPNILQHLKTANNLEFFFPL
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LLCNRTLESMPPGLPSSLMYLSLENNSISSIPEKYFDKLPKLHTLRMSHNKLODIPYNI
FNLPNIVELSVGHNKLKGPYIPRILEHLYLONNEIEKMNLTVMCPSIDPLHYHHLTY
IRVDONKLKEPISSYIFECPPHIHTIYYGEGRSTNGOTIOLKTOVFRRFPDDDDESED
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                                                                              Eukaryoria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ toases 1 to 12414) [ Ohno, I., Matsubara, K. and Okubo, K. Human osteomodulin gene: intron-exon junctions and chromosomal
                                                                                                                                                                            Published Only in DataBase (1997) In press
(pases 1 to 12414)
(hases 1 to 12414)
Ohno,I., Matsubara,K. and Okubo,K.
Direct Submission
Submitted (05-DEC-1997) Ikko Ohno, Institute for Molecular and Cellular Biology, Osaka University, Molecular Genetics; 1-3 Yamada-oka, Suita, Osaka 665, Japan
(E-mail: Kousaku@imcb.osaka-u.ac.jp, Tel:81-6-879-7992,
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                 AB009589.1 GI:2696501
Osteomodulin.
Homo sapiens DNA, clone_lib:lambda FIX II STRATAGENE.
Homo sapiens
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/organism="Homo sapiens"
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Vogell, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P.,
Slightom, J., Schellin, K.A., Kaytes, P.S., Bannigan, C.M., Ruff, V.,
Slightom, J., Schellin, K.A., Kaytes, P.S., Bannigan, C.M., Ruff, V.,
Solita, T. and Huff, R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 107 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
Location/Qualifiers
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contig of 2636 b
gap of unknown liceontig of 2166 b;
app of unknown liceontig of 2221 b;
contig of 2221 b;
gap of unknown liceontig of 2221 b;
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Sequence 107 from Patent W00136473.
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AB009589
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AX147862
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Jurect Submission

Cambridgeshire, CB10 1SA, UK E-mail enquiries:
hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 11, 2002 this sequence version replaced gi:9230935.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em1; EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
http://www.asnace.an be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGp/Chr9
RPI1-7706 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.clori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RP11-77D6 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-77D6 is at 152341 in this sequence. The true left end of clone RP11-1933 is at 123116 in this sequence. The true right end of clone RP11-62C3 is at 2000 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Oryza sativa chromosome 6 clone P0622F03, *** SEQUENCING IN
PROGRESS ***, in ordered pleces.
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/note="Single clone region. Assembly confirmed by
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Oryza sativa
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100.0%; Pred. No. 5.8;
iive 0; Mismatches (
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29058 c 29849 g 50557
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/db_xref="taxon:9606"
/chromosome="9"
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74081. .74116
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/clone="RP11-77D6"
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AP003771.1 GI:14517645
1 (bases 1 to 152341)
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Best Local Similarity 100.
Matches 21; Conservative
                              Ramsay, H.
Direct Submission
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AP003771/c
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                                                                                                                                                                                                                              Direct Submission

Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Oct 17, 2000 this sequence version replaced gi:10277928.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
means.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromsome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Furthar information can be found at http://www.sanger.ac.uk/HGP/Chr13
RP11-168G12 is from the library RPC1-11.1 constructed at the forether details see http://bacpac.med.buffalo.edu/
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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.00.0%; Pred. No. 5.9;
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41119 a 29504 c 30427 g 42370 t
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Best Local Similarity 100.0%; Pr
Matches 21; Conservative 0;
                              AL161422.14 GI:10862741
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                                                                                                                        Homo sapiens
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AL137848/c
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AC024933/c
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Lagran Lagrange (2001) In press

E (bases 1 to 175644)

Sasaki.T. Matsumoto.T. and Yamamoto.K.

Direct Submission

Submitted (20-JUN-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondal
2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasakieabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of I contigs caps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be preserved.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Stone, N.E., Schmutz, J.J., Shang, J., Pennacchio, L.A., Cox, D.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 195384)
Stone, N.E., Schmutz, J.J., Shang, J., Pennacchio, L.A., Cox, D.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-NOV-1999) Department of Genetics, Stanford Human Genome Center, 4005 Miranda Avenue, Palo Alto, CA 94304, USA On Nov 2, 1999 this sequence version replaced 91:5757494.
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Homo sapiens chromosome 4 clone C0494Hll, complete sequence.
AC006499
                                                                              1 (sites)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P06622F03
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Stone, N.E., Schmutz, J.J., Cox, D.R. and Myers, R.M.
Direct Submission
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46662 a 41378 c 40541 g 46713 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="6"
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nes 21; Conservative
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AC006499
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ACO24933 317285 bp DNA linear HTG 06-FEB-2002 Homo sapiens chromosome 3 clone RP11-219D15, WORKING DRAFT SEQUENCE, 27 unordered pleces.
                                                                                                                                                                                                                                                                          /clone_1c0494H11"
/clone_1ib="ROSWELL PARK CANCER RPCI - 11 Human Male BAC
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0%; Score 21; DB 9; Length 195384; Best Local Similarity 100.0%; Pred. No. 5.6; Matches 21; Conservative 0; Mismatches 0; Indels 0;
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.6.
STS Content:
STG-86135 G61558
WI-9872 G05448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC024933.28 GI:18542847
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                       Library"
58996 a 44583 c 41620 g 50185 t
                                                                                                                                                                                                         Location/Qualifiers
1. 195384
7. Crganism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
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                                                                                                                                                                                                                                                                                                                                                                                                                   36 CACCATCTCCCAGGTGATGCC 56
                                                                                                                                                   WI-945 G02751
SHGC-50683 G33721
SHGC-84465 G51855
SHGC-82103 G51922.
                                                                     SHGC-50686 G33724
SHGC-24200 G33354
SHGC-51172 G34253
                                                                                                                         SHGC-51247 G34292
SHGC4-1530 G01882
                                                                                                             WI-4297 G04613
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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 20)
Vogell,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 109 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.0%; Score 21; DB 2; Length 317285; 100.0%; Pred. No. 5.1; ative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                      of 5151 bp in length
to unknown length
of 566 bp in length
f unknown length
of 6798 bp in length
f unknown length
of 6910 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105093: contig of 7789 bp in length
105193: gap of unknown length
115204: contig of 10011 bp in length
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contig of 7292 bp in length
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    .20
    /organism="synthetic construct"

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of 3097 b
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AX147864
AX147864.1 GI:14346860
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/db_xref="taxon:9606"
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        Moser, M., Neal, D., Newtson, N., Mouyen, N., Morsen, M., Neal, D., Newtson, N., Neal, D., Newtson, N., Neytson, N., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pul, L.L., Quilles, M., Ren, Y., Ryues, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S (bases 1 to 317285)

S Worley, K.C.

Direct Submission

L Submitted (03-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Feb 6, 2002 this sequence version replaced gi:15723405.

Center: Baylor College of Medicine

Center: Baylor College of Medicine

Center code: BC/

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu/
  Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.990329
Consensus quality: 299405 bases at least Q40
Consensus quality: 30299 bases at least Q30
Consensus quality: 315960 bases at least Q20
Estimated insert size: 325253; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 7.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 27 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye: 100% of reads
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gap of unknown length
contig of 2035 bp in length
gap of unknown length
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1 (bases 1 to 20)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sojlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 160 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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synthetic construct
artificial sequence.
1 (bases 1 to 48)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.W.
Novel g protein-coupled receptors
Patent: WO 0136473*A 132 25-MAT-2001;
PHARMACIA & UPJOHN COMPANY (US)
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Sequence 160 from Patent WO0136473.
AX147915
AX147915.1 GI:14346910
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Sequence 132 from Patent WO0136473.
AX147887.1 GI:14346882
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/db_xref="taxon:32630"
/note="Novel Sequence"
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artificial sequence.
1 (bases 1 to 2)
Vogeli.G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz., T and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 110 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
Location/Qualifiers
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synthetic construct
artificial sequence.
1 (bases 1 to 20)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Saljitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 131 25-MAY-2001;
PHARMACIA & UPOOHN COMPANY (US)
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/note-"Novel Sequence"
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/organism="synthetic construct"
/db_xref="texon:32630"
/note="Novel Sequence"
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Sequence 110 from Patent WO0136473.
AX147865
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YSTP PROKYNGEQAELKCSPIMOGNEKWAPDSLOGSKLPWRNDPNLTACMAPNNGSD
EPPRGSSMLPPMFROPRFGYEDLOCHKBGSRTSCENFGKHVEKSASCHCTP
VDVYWSKDDKOFAYIWIAIWSILCFFSSAFTYLIFLIDPQRFKYPERPIIFLSMCYCY
YSVGYIIRLESGAESTACDRDSGOLYVIQEGLESTGGTIVFLYLYYFEMASSLWWJIL
TLITMFLAAGKKWGHEAIEANSSYFHLAMAAIPANTIALWWRRAGDELTGLYVGS
MDVNALTGFYLIPLAGCKITGTSFLLGSFVALFHRRVWKTGGENTDKLEKLEKLEWRIGG
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Stark,M.R., Biggs,J.J., Schoenwolf,G.C. and Rao,M.S.
Direct Submission
Submitted (13-JAN-2000) Neurobiology and Anatomy, University of Utah, SO N. Medical Dr., Salt Lake City, UT 84132, USA
Location/Qualifiers
/note="Involved in Wnt signaling, encoding a Wnt-7a
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Stark,M.R., Biggs,J.J., Schoenwolf,G.C. and Rao,M.S.
Characterization of Avian Frizzled Genes in Cranial Placode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF224320 2244 bp mRNA linear VR7 Gallus gallus Frizzled-10 (CFz-10) mRNA, complete cds. AF224320 GI:7340131
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428. :2185
/note="cFz-10"
/note="7-pass transmembrane receptor"
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/dev_stage="stage 4-11 chick"
1. .2244
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/db_xref="G1:7340132"
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Pred. No.
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/product="Frizzled-10"
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100.0%; Pre/
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Best Local Similarity 100.
Matches 20; Conservative
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                              synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 48)
Vogell,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 161 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nohno,T.
Identification of chick frizzled-10 expressed in the developing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawakami, Y., Wada, N., Nishimatsu, S., Komaguchi, C., Noji, S. and
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Gallus gallus Fz-10 mRNA for Frizzled-10, complete cds
AB023806
                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Novel Sequence"
15 c 10 g t
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100.0%; Pred. No. 82;
tive 0; Mismatches
                                                                                                                                    DNA
                                                                                                                               AX147916 48 bp C
Sequence 161 from Patent WO0136473.
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/tissue_type="limb bud"
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256. .2013
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AX147916.1 GI:14346911
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/gene="Fz-10"
256. .2013
/gene="Fz-10"
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Frizzled-10.
48 GGAGTTGCATCAGTGTGGCA 29
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Nohno, T.
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Matches 20; Conservative
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AX147916/c
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/translation="MMFPQSRHSGSSHLPQOLKFTTSDSCDRITDEFQLLQAQYHSLK
LECOKLASRESEMQRHYVYYYEMSYCHNIEMHGAGETWRLNGTCAQVLPYLSQEHQQ
QVLGAIERRAKQYTAPELNSIIRQQLQAHQLSQLQALALPLPTPLPVGLQPPSLFAVSAG
TGLLSLSALGSQAHLSKEDKNGHDGDTHQEDDGEKSD"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria Primates; Catarrhini; Hominidae: Homo.

[ tbases 1 to 37784)
Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhart-Schultz,K.,
Garcia,E., Kyle,A., Ramirez,M., Stilwagen,S., Garnes,J.,
Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A.,
Olsen,A.O. and Carrano,A.V.
Sequence analysis of a 1 Mb region in 19q13.1
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Pred. No.
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/gene="AES"
/number=4
9055. . 9117
/gene="AES"
/number=5
918. . 10920
/gene="AES"
/number=5
10921. . 10995
/gene="AES"
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/gene="AES"
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10996. .11074
/gene="AES"
/number=6
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3347 c 3
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/gene="AES"
/number=2
3144. .6661
/gene="AES"
/number=2
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/number=1
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Best Local Similarity 100.
Matches 20; Conservative
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Hou.E.W. and Li.S.S.-L.

Genomic organization and in situ localization to chromosome 19pl3.3

Genomic AES gene: the gene product exhibiting strong similarity to the amino-terminal domain of Drosophila enhancer of split groucho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession Number to human groucho protein encoded by GenBank Accession Number U04241 and to Drosophila melanogaster groucho protein: Swiss Prot Accession Number P16371; the corresponding mRNA sequence is reported in GenBank Accession Numbers X73357 and X73358"
 FSVLYTVPATCVIACYFYERLNMDYWKIVASQOKCKMNNQTKNLDCMMNNSIPAVEIF
WYRIEMLLYCGITSGMMIWTSKTLQSWQNVCSRRLKKRSRRKPASVITSSGIYKKPQH
PQKRHLAKYESTLQPPA
173 c 606 9 533 t
                                                                                                                                                                                                                                                                                              HSGROUCH2 12524 bp DNA linear PRI 05-JAN-1999 Human groucho protein homolog (AES) gene, exons 2-7 and complete
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join(UBB831.1:1. .59,1. .11296)

/gene="AES"

join(UB831.1:31. .57,3046. .3143,6662. .6725,8426. .8470,

/gene="AES"
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Unpublished
1 (bases 1 to 12524)
Hou,E.W. and Li,S.S.-L.
Direct submission
Submitted (06-FEB-1997) Laboratory of Molecular Genetics, National
Institute of Environmental Health Science, Mail Drop D3-05, P.O.
Box 12233, Research Triangle Park, NC 27709, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 12524)
Miyasaka, H., Choudhury, B.K., Hou, E.W. and Li, S.S.
Molecular cloning and expression of mouse and human cDNA encoding of split groucho protein with strong similarity to Drosophila enhancer cur. J. Blochem. 216 (1), 343-352 (1993)
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9055.2117,10921.10995,11075.>11296)
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                                                                                                    Length 2244;
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/protein_id="AAD00654.1"
/db_xref="G1:4099601"
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2
                                                                                                1.9%; Score 20; DB
100.0%; Pred. No. 42;
Live 0; Mismatches
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/db_xref="taxon:9606"
/chromosome="19"
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1. .12524
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                                                                                                                                                                                                                                                            RESULT 43
HSGROUCH2
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//rpt_family="MER7"
34977. 34965
//rpt_family="MER7"
35188. 35456
//rpt_family="Alu"
35545. 3569
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36861. 36994
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complement(37144. 37245)
/rpt_family="MRR"
                               .18401)
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30963. .30998
/rpt_family="Alu"
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complement(20158...
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/rpt_family="Alu"
complement(21064...
/rpt_family="Alu"
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(1373. .31539
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12970. .23020
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18807. .19120
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10463. 10759
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1056. 11683
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="LL19NCO3 library constructed at LLNL from
flow-sorted chromosomes from hybrid 5HL2-B, which carries
chromosome 19 as its only human chromosome."
2 (bases 1 to 37784)
Lamerdin.J.E.
Direct Submission
Submitted (07-OCT-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Map and sequence oriented from centromere to telomere.
R26667 overlaps PAC PC28130 to the left and cosmid F21426 to the right.
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/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: marginal, score: 49.000"
complement(4383..4678)
complement(4690..4830)
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6150_.6602
.6602
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7409..7685
/rpt_family="Alu"
8018..8305
/rpt_family="Alu"
complement(8423..8722)
                                                                                                                                                                                                                 Location/Qualifiers
1. .37784
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448. .5858
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complement(3631. .3716)
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9988. .10088
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States 1 to 63400)

Birren B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boyuslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Farco, S., Ferrelra, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand Plerre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Levine, R., Liu, G., Maclean, C., Marchas, T., Mehocky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEvan, P., Marquis, N., Mathews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Wail, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rleback, M., Stalley, R., Schauer, S., Schupback, R., Stanan, S., Severti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Vola, N., Wilson, B., Wu, X., Wyman, D., Ye, Wyll, R., Vola, Wilson, B., Wu, X., Wyman, D., Ye, Wyll, R., Vola, Wilson, B., Wu, X., Wyman, D., Ye, Wyll, R., Yola, R., Wilson, B., Wu, X., Wyman, D., Ye, Wyll, R., Yola, Wilson, B., Wu, X., Wyman, D., Ye, Wyll, R., Yola, R., Wilson, B., Wu, X., Wyman, D., Ye, Yeng, R., Yang, R., Wilson, B., Wu, X., Wyman, D., Ye, Yang, J., Yang
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HOMO Sapiens chromosome 8 clone RP11-110116 map 8, LOW-PASS
SEQUENCE SAMPLING.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo, Saplens chromosome 8, clone RP11-110116
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                   Length 37784;
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25;
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   9472
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However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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2006 20703: contig of 708 bp in length 2093 20593: contig of 699 bp in length 2093 20593: contig of 100 bp in length 2093 20593: contig of 699 bp in length 2093 20593: contig of 699 bp in length 2093 20573: contig of 700 bp in length 2010 31300: gap of 1000 bp in length 2010 3209: gap of 1000 bp in length 2010 3210: gap of 1000 bp in length 2010 3224: contig of 700 bp in length 2010 3210: gap of 1000 bp in length 2010 40093: contig of 700 bp in length 2010 40093: gap of 1000 bp in length 2010 5000 40093: gap of 1000 bp in length 2010 5000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 40000 4
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Query Match
1.9%; Score 20; DB 2; Length 63400;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels

Search completed: October 29, 2002, 04:47:09 Job time : 3464 secs

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APPLICATION NUMBER: US/08/664,596B
                                         PCT USSS-1676-30
US-08-967-101-122
US-08-124-698-122
US-09-124-698-122
US-08-146-841C-122
US-08-967-101-73
US-08-967-101-73
US-08-967-101-73
US-08-957-101-73
US-08-957-101-73
US-08-952-541-7
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US-08-496-841C-73
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08664596B Patent No. 5807703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown. Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-824
TELEPHONE: (617) 498-824
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENTH: 433 base pairs
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Treacy, Maurice
Evans, Cheryl
Spaulding, Vikki
Bowman, Michael
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McCoy, John
LaVallie, Edward
Racie, Lisa
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STRANDEDNESS: double
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STATE: Massachus
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-723-462-1

US-08-723-862-1

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US-08-708-541A-31

US-08-708-541A-33

US-08-708-541A-33

US-08-708-541A-33

US-08-708-541A-33

US-08-447-411-75

US-08-487-426-998-3

US-09-426-998-3

US-09-426-998-3

US-09-486-527-30

US-08-487-4268-10

US-08-487-4268-10
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
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US-09-156-425-1/C
Sequence 1, Application US/09156425B
Sequence 1, Application US/09156425B
Patent No. 5952671
GENERAL INFORMATION:
APPLICANT: Baker, Brenda F.
TITLE OF INVENTION: ANTISENSE MODULATION OF FAN EXPRESSION
FILE REPERBACE: RTS-0005
CURRENT APPLICATION NUMBER: US/09/156,425B
CURRENT FILING DATE: 1998-09-18
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100.0%; Pred, No. 11;
1ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                            ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,367
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ored. No. 12;
Mismatches 0
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Pred. No.
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Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-824
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 733 base pairs
TYPE: nucleic acid
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
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Best Local Similarity 100.
Matches 18; Conservative
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; LOCATION: (13)..(2766)
US-09-156-425-1
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LENGTH: 3380
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APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
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ZIP: 02140

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,367
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                                                                            Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-824
TELEFAX: (617) 496-5851
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              Sequence 1, Application US/08738367
Patent No. 5827688
GENERAL INFORMATION:
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LaVallie, Edward
Racie, Lisa
Merberg, David
Treacy, Maurice
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                                                                            Conservative
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STRANDEDNESS: double
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US-08-738-367-1
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APPLICANT:
APPLICANT:
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APPLICANT: Margarit, S. M.
APPLICANT: Margarit, S. M.
APPLICANT: BOTIACK Sjodin, Ann
APPLICANT: BOTIACK
APPLICANT: BOTIACK
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-228M
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 6453;
12;
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12;
                                                                                          | DOCATION: (2042)..(2220) | FEATURE: CDS | LOCATION: (2042)..(2530) | FEATURE: CDS | LOCATION: (2374)..(2533) | FEATURE: CDS | LOCATION: (3321)..(3350) | PUBLICATION: INFORMATION: DATABASE ENTRY DATE: 1991-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 1.7%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 12; Matches 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-09-356-952-8/C
'Sequence 8, Application US/09356952
'Patent No. 6117663
'GENERAL INFORMATION:
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             NAME/KEY: CDS
LOCATION: (1664)..(1774)
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LENGTH: 6453
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; ORGANISM: HOI
US-09-356-952-8
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| Patent No. 6114517 | General No. 6114517 | General Information:
| APPLICANT: Monia, Brett P. | APPLICANT: Xu, Xiaoxing S. | TITLE OF INVENTION: APPLICATION WOMER: US/09/209,668A | CURRENT APPLICATION NUMBER: US/09/209,668A | CURRENT FILING DATE: 1998-12-10 | NUMBER OF SEQ ID NOS: 25 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 10 | LENGTH: 6453 | CURRENT FILING DATE: APPLICATION WORLD | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 10 | SE
                                                  Sequence 14, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STRRET: Two Penn Center, Suite 1800
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION: September 15, 1994
CLASSIFFICATION: 514
PRICE APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               red. No. 12;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MONGCO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 9321-8
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-8383
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERESTICS:
LENGTH: 6453 base pairs
TYPE: nucleic acid
STARNEDDNESS: SIngle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.7%; Sc
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: Innear
US-08-306-6918-14
RESULT 5
US-08-306-691B-14/c
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US-09-209-668-10/c
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Gaps

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0; Gaps
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/product= "Streptococcal plasmin receptor"
/evidence= EXPERIMENTAL
/gene= "plr"
/lumber= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6%; Score 17; DB 1; Length 1125; 0.0%; Pred. No. 37; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start= 115
/function= "High-affinity binding of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: Won Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmin Receptors as
TITLE OF INVENTION: Fibrinolytic Agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSE: David R. Saliwanchik
STREET: 411 N.W. 41st Street, Suite A-1
           CIASSIFICATION: 424
PRIOR APPLICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: UF/S6S-13.C2
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
TELEPHONE: 1125 base pairs
TYPE: NUCLEIC ACID
STREADENESS: Doth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             experimental
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Sequence 1, Application US/08273247

Patent No. 6136323

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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Best Local Similarity 100.'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 TGATTTCCTCCTTATGA 95
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  19920810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide LOCATION: 115..1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATURE:
NAME/KEY: CDS
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         circular
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OTHER INFORMATION:
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TOPOLOGY: cir
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STATE:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFCATION: 435
FILING DATE: Seldman, Stephanle L.
NAME: Seldman, Stephanle L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
TELECHONE: (619) 450-8400
TELECHONE: (619) 450-8400
TELECHONE: (619) 450-8400
SEQUENCE CHARACTERISTICS:
LENGTH: 7898 base pairs
TYPE: nucleic acid
STRANDENNES: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07928462; Batent No. 5328996; Batent No. Applicant: Lottenberg, Richard Applicant: Broder, Christopher C. Applicant: Broder, Christopher C. Applicant: Broder, Christopher C. Applicant: Non Mering, Gregory O. TITLE OF INVENTION: Bacterial Plasmin Receptors as TITLE OF INVENTION: Elbrinolytic Agents: NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: 2 CORRESPONDENCE ADDRESS: 3 ADDRESSE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,462
4250 Executive Square, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Coding Sequence
LOCATION: 249...7307
CTHER INFORMATION:
US-08-984-7098-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4009 AGGCGGAGCAGCAGCTG 3992
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       610 AGGCGGAGGCAGCTG 627
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                  CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32606
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                                                               COUNTRY:
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Sequence 31, Application US/08708541A
Patent No. 581744
GENERAL INFORMATION:
APPLICANT: VAKHARIA, VIkram N.
APPLICANT: WINDT, Egbert
TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: SLIFE 655 Fifteenth Street, N. W.,
STREET: Suite 330 - G Street Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 1935; 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:

COUNTRY: USA

2.TF: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DEACHLIN PC-DOS/MS-DOS

SOFTWARE: PATEM: PC-DOS/MS-DOS

SOFTWARE: PATEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

ATPORNEY/AGENT INFORMATION:

MAME: KITTS, Monica C.

REGISTRATION NUMBER: 36,105

REGISTRATION NUMBER: 36,105

RECISTRATION NUMBER: 36,105

TELEPHONEY/AGENT INFORMATION:

THE TELEPHONEY/AGENT INFORMATION:

TELEPHONEY/AGENT INFORMATION:

TELEPHONEY/AGENT INFORMATION:

TELEPHONEY/AGENT INFORMATION:

THE TELEPHONEY/AGENT INFORMATION:

TELEPHONEY/AGENT INFORMATION:

TELEPHONEY/AGENT INFORMATION:

TELEPHONEY/AGENT INFORMATION:

THE TELEPHONE
                  CURRENT APPLICATION NUMBER: US/09/423,890
CURRENT FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: USSN 60/078,153
PRIOR FILING DATE: 1998-03-16
PRIOR APLICATION NUMBER: USSN 60/099,165
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 17; DB 100.0%; Pred. No. 38; tive 0; Mismatches
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 3264 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              659 GCATGCTGGATCCCCTG 675
CPI-085CPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            812 GCATGCTGGATCCCCTG 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.0ery Match
Best Local Similarity 100.C
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                , NAME/KEY: CDS
; LOCATION: (25)..(1902)
US-09-423-890-5
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LOCATION: 97..531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-708-541A-31/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-708-541A-31
                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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US-09-423-890-5
US-09-423-890-5
Sequence 5, Application US/09423890
Patent No. 6312934
GENERAL INFORMATION:
APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmin(ogen)"
/product="Streptococcal plasmin receptor"
/evidence= EXPERIMENTAL
/gene="plr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6%; Score 17; DB 3; Length 1125;
100.0%; Pred. No. 37;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD: experimental /codon_start= 115 /function= "High-affinity binding of
               ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,247
FILING DATE:
                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: UF/S&S-13.C2
TELECOMMUNICATION INFORMATION:
TELEFHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: M unitypable
INDIVIDUAL ISOLATE: 64/14
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- PLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 115..1122 IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 115..1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: pRL015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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DB 1; Length 4138;
39;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WOEBL, CARL-WILHELM
APPLICANT: REDBHORST, REINHORST
APPLICANT: ROCK, MICHAEL
APPLICANT: ROCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVE
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
                                        ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREES: 175 S. Jefferson Davis Highway, Suite 400 CITY: Arlington
                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6%; Score 17; DB 100.0%; Pred. No. 39; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1755 S. JEFFERSON DAVIS HIGHWAY CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33, Application US/08662227 Patent No. 5922320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEE: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 75
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3149 CAAGCTCAAAATCTGCA 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4138 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              870 CAAGCTCAAAATCTGCA 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                             STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3..4001
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                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-447-411-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-662-227-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: V. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                                                                                                                                                                                                                                                    APPLICANT: VAKENERA, VIKTAM N.
APPLICANT: WANDT, Egbert
TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVIRUS FROM
TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS
CORRESPONDENCE: 34
CORRESPONDENCE ADDRESS:
      Length 3264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3264;
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                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W.,
STREET: Suite 330 - G Street Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER RELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,541A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
38;
Score 17; DB 2;
Pred. No. 38;
               100.0%; Preu. ...
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100.0%; Pred. No. 38;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:

CLASSIFICATION: 424

ATTCHNEY FAGENT INFORMATION:
NAME: KITTS, MONIGE C.
RECISTRATION NUMBER: 36,105

RECISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P8172-6002

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-500

INFORMATION FOR SED ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 3264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: CDNA
      1.6%; Score 17;
                                                                                                                                                                                     RESULT 13
US-08-708-541A-33/C
US-08-708-541A-33/C
Sequence 33, Application US/08708541A
Patent No. 5871744
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-447-411-75; Sequence 75, Application US/08447411 patent No. 5773243; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FRITZINGER, DAVID C. PAPLICANT: BREDEHORST, REINHARD APPLICANT: VOGEL, CARL-WILHELM ITLE OF INVENTION: DNA ENCODING
                                                                                                           2506 CCACATGAAGACCTGGA 2490
                                                                                    126 CCACATGAAGACCTGGA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 CCACATGAAGACCTGGA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 17; Conservative
  Query Match 1.69
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 131..3169
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Suite 33 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
US-08-708-541A-33
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                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09426998

Patent No. 6358706

GENERAL INFORMATION:
APPLICANT: DUBIN, ADERENNE E.
APPLICANT: DAYASHREE
APPLICANT: ZHU, JESSICA Y
APPLICANT: GALINDE, ARK G
APPLICANT: GALINDE, JOSE E
TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
TITLE OF INVENTION: ONE E
TITLE OF INVENTION: 1997
CURRENT APPLICANT: 1999-10-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE PATENTIN VER. 2.0
SEQ ID NO 3
LENGTH: 6822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: DUBIN, ADRIENNE E.
APPLICANT: PYATI, JARASHREE
APPLICANT: ZHU, JESSIAR
APPLICANT: ZHU, JESSIAR
APPLICANT: GALINDE, MARK G.
APPLICANT: GALINDO, JOSE E.
TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
TITLE OF INVENTION: OR E.
TITLE OF INVENTION: ONDER: (ALPHAIG-C)
FILE REFERENCE: ORT-1057
CURRENT APPLICATION NUMBER: US/09/426,998
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: S.
SOFTWARE: PATENTIN VER: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                              Ouery Match 1.6%; Score 17; DB 4; Length 4138; Best Local Similarity 100.0%; Pred. No. 39; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 6822;
39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 17; DB 100.0%; Pred. No. 39; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09426998
Patent No. 6358706
                                                                                                                                                                                                   3149 CAAGCTCAAAATCTGCA 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4561 CTGCTCATTGTGGCCTT 4577
                                                                                                                                                                        870 CAAGCTCAAAATCTGCA 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CTGCTCATTGTGGCCTT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTGCTCATTGTGGCCTT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: HOMO SAPIENS
US-09-426-998-4
                      ; MOLECULE TYPE: CDNA US-09-017-947-33
    linear
  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 4
LENGTH: 7741
                                                                                                                                                                                                                                                                                    RESULT 17
US-09-426-998-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
US-09-426-998-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/09017947
Patent No. 6303754
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: REDEBLORST, REINHORST
APPLICANT: FRIZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,947
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6%; Score 17; DB 2;
100.0%; Pred. No. 39;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
RECISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABLINGTON MALINGTON DAVIS HIGHWAY
                                                                                                                                                                          1126-0107-0X
                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTER.STICS: LENGTH: 4138 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 3149 CAAGCTCAAAATCTGCA 3165
                                                                                                                                                                                                                                                                                             LENGTH: 4138 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           870 CAAGCTCAAAATCTGCA 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 16
US-09-017-947-33
                                                                                                                                                                                                                                                                                                                                                                                                               US-08-662-227-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08487426B
Patent No. 5763173
GENERAL INFORMATION:
APPLICANT: LARRY GOLD
APPLICANT: SUMEDHA JAYASENA
TITLE OF INVENTION: NUCLEIC ACID LIGAND
TITLE OF INVENTION: INHIBITORS TO DNA POLYMERASES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOORDEFICET 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,426B
FILING DATE: 10-JUNE-1995
CLASSIFICATION APPR: APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION NUMBER: 07/536,424
FILING DATE: 11-JUNE-1990
ATTORNEY AGENTE: Z1-OCTOBER: 1992
ATTORNEY AGENTE: Z1-OCTOBER: 1992
ANDAD: CALLOS COURTERED COU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Diane Cruz
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX43-1
TELECOMMUNICATION INFORMATION:
   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (303) 793-3333
TELEPAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                           TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ. ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 30 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 GCTTTTGGGGACATTC 259
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.5
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATY: Denver
STATE: Colorado
COUNTRY: IIS?
ZID.
                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-484-557C-10
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                                                                                                       RESULT 19
US-09-487-368A-226/C
Sequence 226, Application US/09487368A
Patent No. 6261840
GENERAL INFORMATION:
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION:
FILE REFERENCE: RTS-0093
CURRENT APPLICATION NUMBER: US/09/487,368A
CURRENT PAPLICATION NUMBER: US/09/487,368A
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 226
LENGTH: 20
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Sequence 10, Application US/08484557C

GENERAL INFORMATION:
APPLICANT: LARRY GOLD

APPLICANT: SUMEDHA JAYASENA

TITLE OF INVENTION: NUCLEIC ACID LIGAND

TITLE OF INVENTION: INHIBITORS TO DNA POLYMERASES

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.

STREET: 8400 East Prentice Avenue., Suite 200
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ZIP: GOLIII
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,557C
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/596,624
APPLICATION NUMBER: 07/596,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Antisense Oligonucleotide US-09-487-368A-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX43-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
5083 CTGCTCATTGTGGCCTT 5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 TCCTGGGAACAGTGTA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 TCCTGGGAACAGTGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 8400 East
CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Diane Cruz
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US-08-484-557C-10
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Gaps
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Sequence 10, Application US/09258797
Sequence 10, Application US/09258797
Sequence 10, Application US/09258797
SEMENTAL INFORMATION:
APPLICANT: Gald, Larry
TTYLE OF INVENTION: Nucleic Acid Ligand Inhibitors to DNA Polymerases
FILE REFERENCE: NEX 43C/PCT-CIP
CURRENT APPLICATION UNMBER: US/09/258,797
CURRENT FILING DATE: 1999-03-01.
EARLIER APPLICATION NUMBER: 08/945,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                           GENERAL INFORMATION:
APPLICANT: LARRY GOLD
APPLICANT: SUMEDHA JAYASENA
TITLE OF INVENTION: NUCLEIC ACID LIGANDS
TITLE OF INVENTION: THAT BIND TO AND INHIBIT DNA
TITLE OF INVENTION: POLYMERASES
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Ler
1.1e+02;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.5%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US96/09451
FILING DATE: 05-JUNE-1996
APPLICATION NUMBER: 08/487,426
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/487,720
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION NUMBER: 08/484,557
ATTONNEY,AGENT INFORMATION:
NAME: BALTY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: 33,215
REFERENCE/DOCKET NUMBER: 33,215
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPETFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,734
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 10.
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 GCTTTTGGGGACATTC 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                             Colorado
                                                                                                                                                                                                                                                                 ADDRESSEE: Swa
STREET: 8400 E
CITY: Denver
STATE: Colorad
                                                                                                                                                                                                                                                                                                                                                                                         USA
      Patent No. 6020130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-945-734-10
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
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                                                                Gaps
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1.5%; Score 16; DB 1; Length 30; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                   US-08487-720A-10
Sequence 10, Application US/08487720A
Patent No. 5874557
GENERAL INFORMATION:
APPLICANT: LARRY GOLD
APPLICANT: SUMEDHA JORASENA
TITLE OF INVENTION: INHIBITORS TO DNA POLYMERASES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite 200
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: STORAGE
COMPUTER: STORAGE
COMPUTER: OCTORAGE
OF STEATING SYSTEM: MS-DOS
SOFTWARE: WOOTDER: 10.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,720A
FILING DATE: 7-UNE-1995
CLASSIFICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-UNE-1990
PRIOR APPLICATION NUMBER: 07/546,524
FILING DATE: 21-OCTOBER-1992
ATTONNEY/AGENT INFORMATION:
NAME: Diane Cruz
ATTONNEY/AGENT INFORMATION:
NAME: 010 CTUZ
ATTONNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: 33,960

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                                                                                                                    244 GCTTTTGGGGACATTC 259
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Best Local Similarity 100.
Matches 16; Conservative
                     Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                      2 GCTTTTGGGGACATTC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Colorado COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80111
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US-08-945-734-10
   Query Match
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GEMERAL INFORMATION:
GEMERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Cole, Stewart
Stephen
APPLICANT: Gordon, Stephen
TITLE OF INVENTION: HE GENOME OF A MYCOBACTERIUM USING A BAC-PASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3455-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT PILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SEQ ID NO 386
LENGTH: 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: COLe, Stewart
APPLICANT: COLe, Stewart
APPLICANT: COLe, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 740.
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LOCATION: (various positions within the sequence)
COTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-386
                                                                                                                                                                            Gaps
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                                                                                                                         1.5%; Score 16; DB 5; Length 78; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 16; DB 4; Length 99; 100.0%; Pred. No. 1.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 511, Application US/09060756; Patent No. 6183957; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-060-756-386
; Sequence 386, Application US/09060756
; Patent No. 6183957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 ACCCGGGTGGCGGCTG 400
                                                                                                                         Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                         244 GCTTTTGGGGACATTC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                     26 GCTTTTGGGGACATTC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                   linear
          STRANDEDNESS:
                         ; TOPOLOGY: 111;
; MOLECULE TYPE:
PCT-US96-09451-10
                                                                                                                                                                                                                                                                                                                                                                       US-09-060-756-531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us-09-060-756-531
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LENGTH: 99
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                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Sequence
US-09-258-797-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.5%; Score 16; DB 4; Length 78; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application PC/TUS9609451
GENERAL INFORMATION:
APPLICANT: LARRY GOLD
APPLICANT: SUMEDHA JAYASENA
TITLE OF INVENTION: NUCLEIC ACID LICAND INHIBITORS TO
TITLE OF INVENTION: DNA POLYMERASES
NUMBER OF SEQUENCES: 77
CORRESPONDEDE SAMESON and Bratschun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Swanson and Bratschun, L.L.C.
8400 East Prentice Ave., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIF: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BAITY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX43C/PCT
TELECAMUNICATION INFORMATION:
TELEPAN: (303) 793-3333
TELEPAN: (303) 793-3433
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: SUCURED COMPUTER: SUCURED COMPUTER: IBM COMPUTER: OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09451
FILING DATE:
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/487,426
FILING DATE: 7-UNE-1995
PROOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,720
FILING DATE: 7-UNE-1995
PRIOR APPLICATION NUMBER: 08/487,720
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,557
FILING DATE: 7-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: BATTOR 1 INFORMATION:
EARLIER FILING DATE: 1997-10-28
FARLIER APPLICATION NUMBER: 08/487,426
FARLIER PILING DATE: 1995-06-07
FARLIER APPLICATION NUMBER: 08/487,720
FARLIER FILING DATE: 1995-06-07
FEARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 10
LENGTH: 78
LENGTH: 78
                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 GCTTTTGGGGACATTC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 78 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US96-09451-10
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Gaps

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1.5%; Score 16; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 16; DB 5; Length 335;
100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ... crubES.
....ureSSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco COUTY: CA COUNTY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16766
FILING DATE: 12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
PCT-US95-16766-30/C
SEQUENCE 30, APPLICATION PC/TUS9516766
SEQUENCE 30, APPLICATION:
APPLICANT: COLD SPRING HARBOR, LABORALORIS
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON
                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BERTRAM
REGISTRATION NUMBER: 20015
REFREENCE/DOCKET NUMBER: FP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEPAX: 415-398-3249
    REFERENCE/DOCKET NUMBER: A60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               1007 GGCAATGGGATCCCCA 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 GGCAATGGGATCCCCA 20
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-09-060-756-46

i Sequence 46, Application US/09060756

i Sequence 46, Application US/09060756

i Sequence 46, Application US/09060756

i Patent No. 618357

i GENERAL INFORMATION:

APPLICANT: Cole, Stewart

APPLICANT: Gordon, Stephen

APPLICANT: Billault, Alain

TITLE OF INVENTION: HER GRHOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

TITLE OF INVENTION: LIBRARY APPLICATION UP THE DETECTION OF MYCOBACTERIA

TITLE OF INVENTION: LIBRARY APPLICATION OF MYCOBACTERIA

TITLE OF INVENTION: LIBRARY APPLICATION OF MYCOBACTERIA

CURRENT APPLICATION NUMBER: US/09/060,756

CURRENT FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 743

SOFTWARE PATENTING DATE: 2.0
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. OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-46
                                                     Gaps
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1.5%; Score 16; DB 4; Length 287;
100.0%; Pred. No. 1.2e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5%; Score 16; DB 4; Length 315;
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/08576202
Patent No. 6350576
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: U.S.1ESYN, Mikolai
TITLE OF INVENTION: CANCER DETECTION PROBES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: FOUR EMDAICAGERO CENTER, SUITE 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUPUTER REDABLE FORM:
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN RCHEBASE #1.0, Version #1.30
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/576,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REVIAM I BETTAM I
REGISTRATION NUMBER: 20015
                                                                                                                       101 ACCCGGGTGGCGGCTG 116
                                                                                               385 ACCCGGGTGGCGCTG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 ACCCGGGTGGCGCTG 400
                        Best Local Similarity 100.
Matches 16; Conservative
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Matches 16; Conservative
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US-08-576-202-30/c
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LENGTH: 315
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       Query Match
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Sequence 122, Application US/09124698
Sequence 122, Application
General Information:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAULE
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 16; DB 2; Length 440;
100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
         PC-DOS/MS-DOS
n Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
                                                                                                                                            ATTORNEY/AGENT INPORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDENESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-592-541-122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 ATGATCTGCCTGCCTT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
                                                                                                     FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: High
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
US-09-124-698-122
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| Sequence 122, Application US/08592541
| Patent No. 5986054
| GENERAL INFORMATION:
| APPLICANT: ST. GEORGE-HYSLOP, PETER H
| APPLICANT: ROWHENS, DGNAINA M
| APPLICANT: ROWHENS, DGNAINA M
| APPLICANT: ROWHENS, PAUL E
| TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
| NUMBER OF SEQUENCES: 183
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: TESTA, HURWITZ & THIBEAULT
| STREET: High Street Tower - 125 High Street
| CITY: BOSLOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
US-08-967-101-122

Sequence 122, Application US/08967101

Patent No. 5840540

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/AS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 08/592,541
FILING DATE: COMPUTER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.5%; Score 16; DB 2; Lv
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                        ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 122: SEQUENCE CHARACTERISTICS: LENGTH: 440 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: PItcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) US-08-967-101-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 ATGATCTGCCTGCCTT 208
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                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 32
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Petent No. 5840540
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ST. GENCE-HYSLOP, PETER H
APPLICANT: ST. ADULE
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/496,841C

FILING DATE: 28-Jun-1995

CLASSIFICATION: CURROWN>

ATORNEY/AGENT INFORMATION:

NAME: PUT F Fehling*, Ph. D.

RECISTRATION NUMBER: 35,135

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.5%; Score 16; DB 4; Length 440; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFTCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 122:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 122:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 10-NOV-1997
CLASSIFACATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                               STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 ATGATCTGCCTGCCTT 393
                                                                                         STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts: U.S.A.
                                                                      CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: High
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Mass
COUNTRY: U.S
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-496-841C-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 36
US-08-967-101-7
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                                                                                                                                                                                                                                         Sequence 122, Application US/09127480

Patent No. 6194153

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: RASAER, PAULE
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURMITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.5%; Score 16; DB 4; Length 440; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 16; Conservative 0; Mismatches 0; Indels
1.5%; Score 16; DB 3; Length 440; 100.0%; Pred. No. 1.2e+02;
                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 122, Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECHOUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                       193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 ATGATCTGCCTGCCTT 393
                                                                                                                 378 ATGATCTGCCTGCCTT 393
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                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                     Best_Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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US-08-496-841C-122
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US-09-127-480-122
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STATE:
  Query Match
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Gaps

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Sequence 73, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ST. GENEGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: RASER, PAUL E
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                             GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: HIGH Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 16; DB 2; L
100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      ; Sequence 7, Application US/08592541
; Patent No. 5986054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 450 base pairs
nucleic acid
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STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: CDNA
US-08-592-541-7
                                                                                                                                                                                                                                                                                                                 CILL.
STATE: MASSAC...
COUNTRY: U.S.A.
TP: 02110
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Best Local Similarity
Matches 16; Conserv
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STREET: hrz
-mv: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                         STREET: High
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02110
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                                     US-08-592-541-7
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Patent No. 5840540
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
ROMENS, JOHANNA M
APPLICANT:
FRASER, PAUL E
TITLE OF INVENTION:
GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION:
TO ALZHEIMER'S DISEASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.5%; Score 16; DB 2; Length 450; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 Length 450;
                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTE: VAILY
COMPUTE: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION 1435
PION APPLICATION NUMBER: 08/592,541
FILING DATE:
                                                                                                                                                                                                                                                 1.5%; Score 16; DB 2; L
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
               TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 ATGATCTGCCTGCCTT 398
                                                                                                  LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                    193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                                                          383 ATGATCTGCCTGCCTT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                    Query Match 1.5 Best Local Similarity 100. Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                              , MOLECULE TYPE: CDNA US-08-967-101-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                   linear
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Length 450; Indels

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Sequence 73, Application US/09124698
Patent No. 6117978
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENERIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURHIZ & THIBBAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 450;
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7. 1.2e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
Pred. No. 1.2e+02;
: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB;; Pred. No. 1.2e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-127-480-7; Sequence 7, Application US/09127480 Patent No. 6194153; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; SC
illarity 100.0%; P
Conservative 0;
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; MOLECULE TYPE: DNA (genomic)
US-09-124-698-73
  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 ATGATCTGCCTGCCTT 208
                                                                              383 ATGATCTGCCTGCCTT 398
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                                                            193 ATGATCTGCCTGCCTT 208
                      16; Conservative
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hes 16; Conserv
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massach
COUNTRY: U.S.A
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                          RESULT 41
US-09-124-698-73
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Matches
                      Matches
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Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: QALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
STREET: High Street
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                      Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                      DB 2; L6
                                                                                                                                                                                                                                                                                                                                                         1.5%; Scor.
100.0%; Pred. No. 1.-.
... 0; Mismatches
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
                                                FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 248-700
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i: 450 base pairs
nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.5
Best Local Similarity 100.
Matches 16; Conservative
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US-09-124-698-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U ZIP: 02110
                                                                                                                                                                                                                                                                                                                             US-08-592-541-73
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Gaps

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1.5%; Score 16; DB 3; Length 450;

Query Match

Gaps

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Petent No. 6210919
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                               1.5%; Score 16; DB 4; Length 450; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5%; Score 16; DB 4; L. 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | LENGTH + 450 base pairs | LENGTH + 450 base pairs | TYPE: nucleic acid | TYPE: nucleic acid | STRANDEDNESS: single | TOPOLOGY: linear | MOLECULE TYPE: CDNA | SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-08-496-841C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby, & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlmer, Ph.D.
REGISTRATION NUMBER: 35.135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 7:
             TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-127-480-73
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.'
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                     193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                                                             383 ATGATCTGCCTGCCTT 398
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COUNTRY: U.S.A.
ZIP: 10022
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Matches 16; Conserve
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US-08-496-841C-7
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APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 450;
                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2e+02;
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5%; Score 16; DB 4;
100.0%; Pred. No. 1.2e+0;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: High Street Tower - 125 High Street CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/127,480 FILING DATE:
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHRRACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.1
Matches 16; Conservative
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                                                         Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-09-127-480-7
                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
               STREET: High
                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-127-480-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 43
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Gaps

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US-06-496-941C-73

US-06-496-941
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Search completed: October 29, 2002, 03:50:18 Job time : 122 secs

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Gencore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2002, 03:24:48; Search time 1727 Seconds

(without alignments)

8135.686 Million cell updates/sec

Title: US-09-886-041-1

Sequence: 1atgacaacgggtcgtgctg.....acattgttgagtggcactga 1041

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size: 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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1: em\_estba:\*
2: em\_esthum:\*
3: em\_estin:\*
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8: em\_estro:\*
9: gb\_est1:\*
10: gb\_est2:\*
11: gb\_htc:\*
12: gb\_gss:\*
13: em\_gss\_hum:\*
14: em\_gss\_hum:\*
15: em\_gss\_pln:\*
16: em\_gss\_vrt:\*

summaries

Post-processing: Listing first 45

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AF345568 Homo sapi	N62053 EST52h035 W	AG114987 Pan trodl	BG677418 602625245	AW378847 PM0-HT022	BG260219 602371328	BB849390 BB849390	AG106513 Pan troql	AW876644 CM1-PT003	AV734147 AV734147	AA659324 nul3c07.s	AQ401655 HS_5044_B	AQ637267 RPCI-11-4	BG813280 daf73b11.	AA220849 mv69d05.r	BG823216 602726580	BG823067 602728095
	ID	AF345568	N62053	AG114987	BG677418	AW378847	BG260219	BB849390	AG106513	AW876644	AV734147	AA659324	AQ401655	AQ637267	BG813280	AA220849	BG823216	BG823067
	ОВ	=	10	13	10	σ	ដ	σ	12	6	6	σ	17	12	10	σ	10	10
	Query Match Length DB	1372	306	680	852	209	546	422	665	119	396	507	509	528	544	654	879	948
æ	Query	100.0	3.1	3.1	3.1	3.0	3.0	2.8	2.5	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9
	Score	1041	32	32	32	31	31	29	23	20	20	20	20	50	20	20	20	20
	Result No.	П	7	9 9	4	S	9	7	ω υ	6 0	10	11	12	13	c 14	15	c 16	c 17

AL237908 Tetraodon AQ426903 CITBLED: AQ069550 HS_2033 AQ069550 HS_2057_B BE846821 UV90b09;Y AW528652 UI *R*ET1- AT981199 pat. PK*044 AA526211 N159c06.5 BE4778693 163050 BA AI51066 vx91c7,Y BC995639 PAZ-HT034 BG642257 3B5 Droso BH190810 TC3-39E7. B79552 CIT-HSP-204 AQ62105 HS_2142_B AA169173 Zp20c12.5 AA169173 Zp20c12.5 AA169173 Zp20c12.5 AA169173 Zp20c12.5 AA169173 Zp20c12.5 AA169173 Zp20c12.5 AA169173 Zp20c12.5 AA169173 Zp20c12.5 AA169173 Zp20c12.5 AA169173 Zp20c12.5 AA239913 RPCI-23-7 AA239913 RPCI-23-7 AA239913 RPCI-23-7 AA231947 CLS447 CL BC77745 CLS447 CL BC77745 CLS447 CL	SINIS	ens putative chemokine receptor (FKSG80) mRNA, complete  1 GI:13517963  ens;  Wetazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Eutheria: Primates; Catarrhini; Hominidae; Homo.  1 to 1372)  and Gong,L.  cloning of FKSG80, a novel gene encoding a putative receptor  receptor  1 to 1372)  bmission  (106-FEB-2001) Beijing FENGKESHENG Function Gene (106-FEB-2001) Beijing FENGKESHENG Function Gene (106-FEB-2001) Beijing receptor  cation/Qualifiers  1 to 1372)  consistent and consist
CNSO3CKB AQ26903 AQ26903 AQ37023 AQ069550 BER48821 AY281562 AY281562 AA526211 BEG7257 BEG7257 BEG7257 BEG7257 BEG7257 BEG7257 BEG7257 BEG7059 AA866830	ALIGNMENTS	1372 bp ve chemokine 7963 Chordata; Cr Primates; Ca 'L. f FKSG80, a n in Tao Lu C Tou Tiao Lu C Tou Tiao Lu C China ualifiers "Homo sapiens taxon:9606" G80" G80" G80" G1:13517964" G1:13517964" G1:13517964" G81:13517964"
120 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		11/96 11/96
1 101 101 2005 33008 33008 33008 444 441 441 441 441 441 441 441 441 44		aplens putative chee 68 68.1 GI:13517963 aplens cta; Metazoa; Chord ais Eutheria; Prima ses 1 to 1372 1ar cloning of FKSG inc receptor ished ses 1 to 1372 ses 1 to 1372 ses 1 to 1372 cybnission receptor 1372 cybnission receptor ished for FEB-2001) B logy Ltd. 4 Tou Til 10050, P.R. Chin Location/Qualifi 1. 1372 chromosome="12" 1. 1372 forcanism="Homo /db_xref="ExSG80" /gene="FKSG80" /gene="FKSG
		5568 5568. 7. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.
		WHO WE STORED THE STORES
000 0 00 0 00 0 00 00 00 00 00 00 00 00		RESULT 1 ACT45568 LOCUS DEFINITION ACCESION VERSION KEYWORDS SOURCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL GENTURES COURCE COS COS

Euteleostom1;

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/clone="52h035"
/clone="1b="WATMA"
/clone=lib="WATMA"
/note="Vector: lambda gtll; Site_1: EcoRI; White adipose tissue, sub cutaneous, adult, female. Purification of polyA mRNA, first strand priming with random oligonucleotides. Ligation of adaptors EcoRI/NotI, cloning in EcoRI site of lambda gtll."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes DNA, clone: PTB-122B10.F, genomic survey sequence. AG114987
AG114987
GGIS, GGS (genome survey sequence).
Fan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-122B10.F.
Fan troglodytes
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                            N62053 306 bp mRNA linear EST 12-JUN-1996 EST52N035 WATM1 Homo sapiens cDNA clone 52N035 similar to gb HSHM74 G protein-coupled receptor family, mRNA sequence.
      Bouillaud, F. 2000, Study of expressed sequences tags in adipose tissue 1995 Unpublished (1995) Contact: Frederic Bouillaud Centre de Recherche sur l'Endocrinologie moleculaire et l
                                                                                                                                                                                                                                             Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                               amplified insert,
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Pred. No. 2.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                               9, Rue Jules Hetzel, Meudon Bell
Tel: 33 1 45 07 52 87
Fax: 33 1 45 07 58 90
Email: bouillau@infobiogen.fr
automatic cycle sequencing of Pc
putative coding sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCAGCTTCACCTACATGAACAGCATGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
                                                                                                                                                                                                                                            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain-"caucasian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.1%; Scur.
100.0%; Pre
                                                                        CACATTGTTGAGTGGCACTGA 1041
                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 306)
                                                                                                                                                                                             N62053.1 GI:1209207
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                                                                                                                                                                                                                      human.
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Best Local S
                                                                                                                      RESULT 2
N62053
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
AG114987/C
LOCUS
DEFINITION
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ORIGIN
                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
COMMENT
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Matches
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VERSION
KEYWORDS
SOURCE
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                                                                                  1162
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Length 852;

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/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="bull00 (T1 phage-resistant)
/lab_host="bull00 (T1 phage-resistant)
/note="Organ: skin; Vector: pcWV-SPORT6; Site_1: Not!;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                        3.1%; Score 32; DB 10; 1 100.0%; Pred. No. 2.9e-05; Live 0; Mismatches 0;
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/clone="IMAGE:4750187"
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                                                                                                                                                       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehikro-chhou, Tsurumi - ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG677418 852 bp mRNA linear EST 01-MAY-2001 602625245F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750187 5',
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
row: j column: 12
High quality sequence stop: 826.
Location/Qualifiers
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                           2 (bases 1 to 680)
Fullyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totchi,Y., Watenabe,H. and Sakaki,Y.
Direct Submission
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-122810.F"
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/db_xref="taxon:9606"
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//drganism="Homo sapiens"
//db_xref="taxon:9506"
//db_xref="taxon:9506"
//db_xref="taxon:9506"
//db_xref="taxon:9506"
//db_xref="taxon:0506"
//db_xref="
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMOst2=PMO-HT0228-
181099-001-0408&t3=1999-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence start: 10
Location/Oualifiers
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AW378847 200 Dp mRNA linear EST 04-FEB-200 PMO-HT0228-181099-001-d08 HT0228 Homo sapiens CDNA, mRNA sequence. AW378847
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludvig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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HGGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project Unpublished (1999)
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llarity 100.0%; Pred. No. 6.6e-05;
Conservative 0; Mismatches 0;
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MIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara K., T. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-111A21.F.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes DNA, clone: PTB-111A21.F, genomic survey sequence.
AGL06513
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                 Fax: 01-73-70-321.
Fax: 01-73-70-9210-9210
URL:http://genome-gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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penes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                      Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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109 c 119 g 114 t
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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100.0%; Pred. No. 0.00088;
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/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
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/clone="IMAGE:479391"
/clone="IMAGE:479391"
/clone="IMAGE:479391"
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/lab_host="IM108 (phage-resistant)"
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Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHLMGC Library."
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BB849390
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Akimura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Satto, R., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
                                                                                                        BG260219 546 bp mRNA linear EST 13-FEB-2001
602371328Fl NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4479391 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10311 row: g column: 08
High quality sequence stop: 546.
Location/Qualifiers
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Length 119;

DB 9;

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1...19
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13 a 46 c 31 g 29 t
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      High quality sequence stop: 113.
Location/Qualifiers
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC):

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Clones are derived from the chimpanzee BAC library PTB This BAC end clone are derived from the chimpanzee BAC library PTB This BAC end clone tracking errors.
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1 (bases I to 119)

1 blass Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-PT0030-170
100-096-f09&t3=2000-01-17&t4=1)
Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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/clone_lib="PTB Chimpanzee Male BAC Library"
| 187 c 157 g 137 t 3 others
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-111A21.F"
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Yangy Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z. and Han, Z. and Han, Z. and Lange collaboration of the complete collaboration of the complete collaboration of the colla
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
AV734147 cdA Homo sapiens cDNA clone cdAAUC10 5', mRNA sequence.
AV734147
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Chinese National Human Genome Center at Shanghai
SJG Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801929
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100.0%; Pred. No. 42;
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This clone is available at CHGC in Shanghai.
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/dev_stage="Adult"
/lab_host="BM25.8"
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/db_xref="taxon:9606"
/clone="cdAAUC10"
/clone=lib="cdA"
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High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Gl6-368 Gl6-3687 Eax: (206) 616-3887 Ext. (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" 3 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
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Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
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Map Building
                                                                                                           Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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/db_xref="texon:9606"
/clone="Piate=650 Col=23 Row=B"
/clone_lib="RPCI-11 Human Male BAC Library"
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Other_GSSs: RPCI-11-479K17.TJ
Other_GSSs: RPCI-11-479K17.TJ
Ochtact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
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Location/Qualiflers
1. .509
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AQ637267
AQ637267.1 GI:5099902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Tissue Procurement: W. D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Anote="Vector: pawpl0; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 mcrodisseted preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pawP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                        AA659324 102-CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1207884 similar to contains Alu repetitive element;, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 507)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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S09 bp DNA linear GSS 13-MAI HS.5044_B1_A12_T7 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=620 Col=23 Row=B, DNA sequence.
AQ401655.1 GI:4409993
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AA659324.1 GI:2595478
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Best Local Similarity 100.0
Matches 20; Conservative
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AQ401655
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AA220849
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: Info@lmage.llnl.gov

Possible reversed clone: similarity on wrong strand

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amopodinae; Xenopus:

1 (bases 1 to 544)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wyller, Underwood,K., Theising,B., Bowers,Y., Person, B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R., Ritter,E., Jackson,Y., McCann,R., Washu Xenopus EST project, 1999
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BGB13280
4273b1.y1 NICHD XGC Eyel Xenopus laevis cDNA clone IMAGE:4755429
5, similar to TR:Q06744 WHC CLASS II HISTOCOMPATIBILITY
ANTIGEN, BETA CHAIN PRECURSOR ;, MRNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                         Email: hbe@filgr.corg
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: T7
Class: BAC ends.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Lymphocytes"
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
156 c 140 g 93 t l others
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Fax: 314 286 1810
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Medical Center Dr., Rockville, MD 20850
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100.0%; Pred. No. 46;
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
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/db_xref="taxon:9606"
/clone="RPCI-11-479K17"
/clone_llb="RPCI-11"
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                   301 838 0200
301 838 0208
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/clone_lib="NICHD XGC Eyel"
/clone_lib="NICHD XGC Eyel"
/dev_stage="adult"
/lab_host="OHIOB (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_l: NotI;
/stage insert size 2.3 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 654)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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AA220849

MRNA linear EST 10-FEB-1997

MWG9G05.r1 Soares mouse 3NME12 5 Mus musculus cDNA clone

IMAGE:660297 5' similar to qb:X15334_rnal CREATINE KINASE, B CHAIN

(HUMAN); gb:M7449 Mouse creatine kinase B gene, complete cds

(MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 10-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1990)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                  DB 10; Length 544;
46;
                                                                                                                                                                                                                                                                                                                                                 0; Indels
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="InAGE:660297"
/clone="InAGE:660297"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 216.
Location/Qualifiers
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100.0%; Pre
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Best Local Similarity 100.0
Matches 20; Conservative
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BG823216/c DEFINITION

ACCESSION

VERSION KEYWORDS

RESULT 16

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ORIGIN

ORGANISM

SOURCE

AUTHORS

REFERENCE

JOURNAL

COMMENT

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AL237908.1 G:7897043
AL237908.1 G:7897043
AL237908.1 G:7897043
GSS; genome survey sequence.
GSS; genome survey sequence.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
El (Dases 1 to 1016)
Roest-Crollius, H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Shouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
Charaterization and repeat analysis of the compact genome of the
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1016 bp DNA linear GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
014H16 of library G from Tetraodon nigroviridis, genomic survey
sequence.
BG823067 948 bp mRNA linear EST 22-MAY-2001
602728095F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4867774 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Arc.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NiH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1736 row: m column: 23
High quality Sequence stop: 722.
High quality Sequence stop: 722.
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 94). Nattonal trip://mgc.nci.nih.gov/.
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100.0%; Pre
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CNS03CKB/c
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1. 879
/ Organism="Homo sapiens"
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/clone="IMAGE:4866283"
/clone="IMAGE:4866283"
/clone="IMAGE:4866283"
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        adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.G.E. Consortium/LLNL at:
http://mage.lnh.gov
Plate: LLCM1732 row: o column: 20
High quality sequence stop: 797.
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11H-MGC http://mgc.nci.nih.gov/. National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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100.0%; Pred. No. 52;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         1.9%; Score 20; DB 9; Length 654;
Llarity 100.0%; Pred. No. 48;
Conservative 0; Mismatches 0; Indels
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RESULT 17 BG823067/c

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Gaps

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us-09-886-041-1.olig.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 267)

Konno, H., Alzawa K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota K., Kagawa, I., Kai,
C., Kawai, J., Kikuchi, N., Kojima, Y., Koda, S., Kusakabe, M., Alatuyama, T., Miki, R., Mizuno, Y., Natamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Soqabe, Y., Suqahara, Y., Suzuki, H.,
Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y.,
Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
Yoshiki, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Unpublished (1999)

NL Contact: Yoshihde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV237023 RIKEN full-length enriched, 10 day neonate skin Mus musculus cDNA clone 4732417M09 3' similar to 214044 M.musculus mrNA AV237023 RAUSTONE AV237023
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URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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CalTech Human BAC Library D"
36 q 34 t
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                                                                                                                                                                                                                  Length 152,
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1.1e+02;
                                                                                                                                                                                                                  Query Match 1.8%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 19; Conservative 0; Mismatches
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AV237023/c
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L Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

http://www.genoscope.cns.fr/Tetraodon.

cocation/Qualifiers

l. 1016
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/clone="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 152)
S zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
L Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ426903 15272H23.TF CITBI-E1 Homo saplens genomic clone 2572H23,
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Mil 21
Class: BAC ends.
                                                                         2 (bases 1 to 1016)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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          freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.9%; Score 20; DB
100.0%; Pred. No. 54;
tive 0; Mismatches
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/db_xref="taxon:9606"
/clone="2572H23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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AQ426903.1 GI:4499539
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                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 1016)
Genoscope.
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Best Local Similarity
                                                 Unpublished
                                                                                                                                                                                                                                                                                     Unpublished
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AQ426903/c
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Gaps

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uv90b09.yl Soares mouse 3NbMS Mus musculus cDNA clone LMAGE:34144255', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I bases 1 to 302)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available robeity-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                 Length 268;
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0; Indels
                                                                                 Indels
                                               DB 12; L
. 1.3e+02;
ches 0;
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/clone_lib="Soares mouse 3NbMS"
                                        1.8%; bccd. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Mismatches
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Mus musculus"/strain-"C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: -40RP from Glbco
High quality sequence stop: 286.
Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH108"
 56 9
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                                                                                                                                  164 CCTTATGATCTGCCTGCCT 182
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Unpublished (1997)
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Best Local Similarity 100.0
Matches 19; Conservative
                                                                  Best Local Similarity 100.
Matches 19; Conservative
 78
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                                                      168 bp DNA linear GSS 04-AUG-1998 sapiens genomic clone Plate-2267 Col-22 Row-F, DNA sequence. AQ069550.1 GI:3384749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 268) Mahalaas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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/db_xref="taxon:9606"
/clone="Plate=2267 Col=22 Row=F"
/clone=_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Col1 DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                               Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 19; DB 9; La
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0;
                /tissue_type="skin"
/dev_stage="10 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 268.
Location/Qualifiers
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Plate: 2267 row: F column: 22
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                665 TCATGGTGGTGGCAATTGT 683
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Gaps

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CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing Center Clone distribution: NGI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/Image/image.html
Insart Length: 491 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 05-AUG-1997
                                                                                                                             Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi; Archosauria: Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 378)
1 (bases 1 to 378)
2 Trunnagaruv V.G., Sofer,L., Cui,J. and Burnside,J. An expressed sequence tag database of T-cell-enriched activated chicken splenocytes: sequence analysis of 5251 clones 20318616
Contact: Joan Burnside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 396)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 bp mRNA linear EST 05-AU ni59c06.sl NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:981130 similar to contains Alu repetitive element;, mRNA sequence. AA526211. AR526211.1 GI:2268280 EST.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: capubs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Con A-activated splenic T cell"
/lab_nost="E.coll TOP10 F'"
/note="Vector: pcDNA3"
50 c 84 g 108 t 20 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /.organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pat.pk0048.b5.f"
/clone_libb"chicken activated T cell cDNA"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 19; DB 9; Length 378; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3341
Email: joan@UDel.Edu, www.chickest.udel.edu
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                             AI981199.1 GI:5884227
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Matches 19; Conservative
                                                                                                        Gallus gallus
                                                                                chicken.
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/db_xref="taxon:1016"
/clone="Ul-R-BT1-ako-q-08-0-Ul"
/clone="Ul-R-BT1-ako-q-08-0-Ul"
/clone="Ul-R-BT1-ako-q-08-0-Ul"
/clone="Ul-R-BT1-ako-q-08-0-Ul"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/dev_vector: p773D-Pec (Pharmacia) with a modified
/note="Vector: p773D-Pec (Pharmacia) with a mixture of
the following tissues: hippocampus, thalamus, mid-brain,
medulla, corpus striatum, cerebral cortex and testis. For
a detailed description of the library from which this
clone was derived, phease visit our web site at
ratest.eng.ulowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-BT1
TAG_LIB=UI-R-BT1
TAG_LIB=UI-R-BT1
TAG_LIB=UI-R-BT1
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                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dr track served to identify it as a clone from the normalized corpus-striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive belements were found in this cDNA sequence: 25-49, septimer: Mil Forward POLYA-Yes.
                                                                                                                                                                                                                                                        Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 B250
Fax: 319 335 9565
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
UI-R-BT1-ako-g-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.ulowa.edu
                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
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                                                     AW528562.1 GI:7170976
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                        Norway rat.
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AUTHORS
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SOURCE
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Gaps

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3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr7r3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                              AI510676 417 bp mRNA linear EST 12-MAR-1999 vx91c07.yl Soares_thymus_2NbMT Mus musculus cDNA clone iMAGE:1282572 5', mRNA sequence.
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PMZ-HT0342-190201-008-b04 HT0342 Homo sapiens cDNA, mRNA sequence.
BG995639
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Seq primer: -40RP from Gibco
High quality sequence stop: 402.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 417)

NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                         Gaps
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Pred. No. 1.4e+02;
  Pred. No. 1.4e+02; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_thymus_2NbMT"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1282572"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
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100.0%; Pred
0; N
                    ö
100.08;
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                                                            855 TCCCAAATTCTACAACAAG 873
                                                                                                    205 TCCCAAATTCTACAACAAG 187
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  Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity
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ACCESSION
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A1510676/c
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AUTHORS
TITLE
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BG995639
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KEYWORDS
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Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library.

Unpublished (2000)

Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single pass sequencing. Bases called and alt_trimmed with phred v0.980904. Wettor identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 28-AUG-2000
                                                                                                                                                                             /note-rector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 56.5380-5181. (1996) Cancer Research 56.5380-5181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 399)
Sonstegard, T.S., Capuco, A.V., Van Tassell, C.P., Ashwell, M.S. and
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                Length 396;
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                                                                                                                                                                                                                                                                                                                                            Ouery Match 1.8%; Score 19; DB 9; Length 396
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                         /clone IMAGE:98130 /clone IIMAGE:98130 /clone_lib="NCI_CGAP_Ov2" /tissue_type="covary" /lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112
                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l. .399
/organism="Bos taurus"
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/clone_lib="BARC_5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Plate: 8 row: D column: 18
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tads@lpsi.barc.usda.gov
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Location/Qualifiers
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BE478693.1 GI:9598226
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BE478693/c
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Evolutionary EST analysis identifies rapidly evolving male
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BH190810.1 GI:16358086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: head_neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

71 c 108 g 108 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-HT0342-
190201-008-bbd&&13=2001-02-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 408.
                                                                                  Burartotta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 437)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Matsukuma,A., Baia,G.S., Simpson,D.H., Matsukuma,A., Bordin,S., Costa,F.F., Matsukuma,A., Bordin,S., Costa,F.F., Matsukuma,A., Bordin,S., Costa,F.F., Matsukuma,A., Goldiveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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441 bp mRNA linear EST 21-JUN-2001
3B5 Drosophila accessory gland pSport1 library Drosophila simulans
                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila simulans.
Drosophila simulans
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 441)
Swanson, W.J., Clark, A.G., Waldrip-Dail, H.M., Wolfner, M.F. and Aquadro, C.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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20202663
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100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0342"
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BG642257
BG642257.1 GI:14522113
  BG995639.1 GI:14399709
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                                                                                                                                                                                                                                                                                                                       sequence tags
                                                                    Homo sapiens
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BG642257/c
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Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seg primer: M13 Rev
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH190810 458 bp DNA linear GSS 24-OCT-2001
TC3-39E7.TR TC3 Trypanosoma cruzi genomic clone TC3-39E7, DNA
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/db_xref="taxon:5693"
/clone="TC3-39E7"
/clone_Ib="TC3-39E7"
/note="Vector: pBeloBAC11; Site_1: Hin dIII; Constructed for Uppsala University by Marie-Christine Le Paslier in
                                                                                                                                                                                                                           /organism="Drosophila simulans"
/db_xref="taxon:7240"
/clone_lib="Drosophila accessory gland pSport1 library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
reproductive proteins in Drosophila
Proc. Natl. Acad. Sci. U. S. A. 98 (13), 7375-7379 (2001)
21309955
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                Contact: Swanson WJ
Molecular Biology and Genetics
Cornell University
Cornell University
Tel: 607 254 4839
Fax: 607 255 6240
Email: wjs18@cornell.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 441;
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                                                                                                                                                                                                                                                                                                                                                                  /note="Dissected accessory glands"
92 c 116 g 104 t 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 10; I
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                           /tissue_type="accessory gland"
/cell_type="reproductive"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cruzi"
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                                                                                                                                                                                                Location/Qualifiers
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127
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KEYWORDS
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AW928794/C
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                        RESULT 32
AQ682105/c
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I. (bases 1 to 463)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Lu Unpublished (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
the laboratory of Denis Le Paslier at the Centre d'Etude du Polymorphisme Humain (CEPH), Paris, France. Briefly, Trypanosoma cruzi C.Brener agarose embedded DNA (obtained from Dr. Franco da Silveira) was partially digested with Hin dIII. High molecular weight fragments were ligated in plealobacil digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 33 X the haploid genome."
                                                                                                                                                                                                                                                                                                                                                                                                    B79552 4-0CT-1998 CIT-HSP Homo sapiens genomic clone 2042N4, DNA sequence.
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Mil Reverse
Class: BAC ends.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Pred. No. 1.5e+02;
0; Mismatches 0;
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/db_xref="GDB:7053631"
/db_xref="taxon:9606"
                                                                                                                                               126 g
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="2042N4"
                                                                                                                                                                                                                                                                            611 GGCGGAGGCAGCTGGC 629
                                                                                                                                                                                                                                                                                                 146 GGCGGAGCAGCAGCTGGC 164
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B79552.1 GI:2866575
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Best Local Similarity
Matches 19; Conserv
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B79552/c
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TGGTGGTGCAATTGTGTT 686

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
AQ682105 480 bp DNA linear GSS 28-JUN-1999 HS_2142_B2_202_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2142 Col=4 Row=N, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW928794 tomato flower buds 8 mm to pre-anthesis, Cornell University Lycopersicon esculentum cDNA clone cTOC3K1 5', mRNA
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1 (bases 1 to 481)
van der Hoeven, R.S., Bezzerides, J.l., Matern, A.L., Holt, I.E., Liang, van der Hoeven, R.S., Graven, M.B., Bowman, C.L., Ahn, S., Ronning, F., Upton, J., Hansen, T., Craven, M.B.,
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
High Throughhut Sequencing Center
University of Washington
10 incersity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallacedu.washington.edu
Clones may be purchased from Research Genetics (Info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Seq primer: MIJ3 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
Adb_wref="teaxon:9606"
/clone="plate=2142 Col=4 Row=N"
/clone="lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ģte-"Organ: sperm; Vector: pBeloBAC11; BAC Clones in
€oli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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100.0%; Pred. No. 1.5e+02;
ative 0; Mismatches 0; Indels
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                                                                                                                A0682105.1 GI:5258088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 TGGTGGTGCCAATTGTGTT 11
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AW928794
AW928794.1
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99380589
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Best Local Similarity
Matches 19; Conserv
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Page 15

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/clone="IMAGE:610006"
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AA866830/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 482)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL69173 tratagene fetal retina 937202 Homo sapiens CDNA Clone IMAGE:610006 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
,C.M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D. Generation of ESTs from tomato flower tissue
                                                                                                                                                                                                                                                                                                                                        /tissue_type="flower"
/dev_stage="buds 8mm-to-preanthesis"
/dev_stage="buds 8mm-to-preanthesis"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 26 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
IMAGE Concertium (info@image.llnl.gov) for further information.
Seg primer: -40MJ3 fwd. from Amersham
High quality sequence stop: 404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                   /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="TCO3K1"
/clone="TCO3K1"
/clone=lib="tomato flower buds 8 mm to pre-anthesis,
Cornell University"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                              Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
                                                                               Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:4625265"
/db_xref="taxon:9606"
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AA169173.1 GI:1747749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.v
                                       Unpublished (1999)
Contact: CUGI
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AA169173
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

(a) (bases 1 to 496)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wile,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

(I) (mpublished (1996)

(I) (mpublished (1996)

(Contact: Marra M/Mouse EST Project
(WashU-HHMI Mouse EST Project
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(WashU-HHMI Mouse EST Project
(WashU-HMI Mouse EST Proj
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 16-MAR-1998
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA866830 496 bp mRNA linear EST vx91c07.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1282572 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 19; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 491.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   851 CCTTTCCCAAATTCTACAA 869
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EST 28-DEC-2001

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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Bmail: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 bp DNA linear GSS 15-JUN-2000 PROLI-23-42F8.TV RPCI-23 Mus musculus genomic clone RPCI-23-42F8, AZ253634
                                                                                                                                                                                                                                                               1 (bases 1 to 509)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Fertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 515)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 509;
                                       BM287008 509 bp mRNA linear 527250 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .509 //
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 135 row: J column: 23
Seq primer: ATTFAGGTGACACTATAG.
Location/Qualifiers
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                                                                                        BM287008
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                                                                                                                                                         COW.
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RESULT 37
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                                                                                                                                                                                                                                                                                                                                  AZ747765 508 bp DNA linear GSS 25-JAN-2001
RPCI-24-99M13.TJ RPCI-24 Mus musculus genomic clone RPCI-24-99M13,
DNA sequence.
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Russell,D., de Jong.P. and Fraser,C.M.
Whouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other.GSSs: RPCI-4-99M13.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
TTel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: stlato@tylor.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdeJong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tjgr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 99 row: M column: 13
Seq primer: SP6
Class: BAC ends.
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/cell_type="Spleen/Brain"
/cote="Vector: pTARBACL; Site_1: BamH1; Site_2: BamH1;
/ROC1-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 508)
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                                                                                     Length 496;
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
                                                                                   Query Match 1.8%; Score 19; DB 9; L. Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 19; Conservative 0; Mismatches 0;
Soares and M.Fatima Bonaldo."
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1. .508
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="RPCI-24-99M13"
/clone_lib="RPCI-24"
/sex="Male"
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                                                                                                                                                                           422 CCCTGGTCATCCTGGGAAC 440
                                                                                                                                                                                                   287 CCTGGTCATCCTGGGAAC 269
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JOURNAL
COMMENT
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AZ747765
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KEYWORDS
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Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                     Tel: 314 286 1800
Fax: 314 286 1810
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AQ535999/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
Cool: Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BH10B electrocompetent cells (BRL Life Technologies). "
126 c 100 g 138 t
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                                                                                                                                                                                                                            Email: szhoottigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pletez'édejong, med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
  Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA180359 519 518 bp mRNA linear EST 31-DEC-199 zp15907.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone mAAE:609564 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                     Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Cohter_GSSS: RPCI-23-42F8 TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
FEX: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
/lab_host="DH10B"
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AA180359.1 GI:1761641
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Best Local Similarity 100.0
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Class: BAC ends.
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AL Unpublished (1997)

Other_GSSs: RPCI-11-318M7.TV

Other_GSSs: RPCI-11-318M7.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

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Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: bbeetigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from RACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6

Class: BAC ends.
Email: estGwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE consortum (info@image.llnl.gov) for further information.
Seq primer: -40ML3 fwd. from Amersham
High quality sequence stop: 382.
Location/Qualifiers
1. 518
Auref="60814624823"
Ab_rref="60814624823"
Ab_rref="60814624823"
Ab_rref="6081646"
Clone="lb="strategene fetal retina 937202"
Action="lb="strategene fetal retina 937202"
Action="lb="strategene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 518)
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/db_xref="GDB:7622022"
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Indels

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Best Local Similarity 100.
Matches 19; Conservative
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House mouse.

Mas musculus

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryote; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 545)

I (bases 1 to 545)

I (bases 1 to 545)

Sabo,S., Nlerman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret

B., Levins,W., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.

and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-23

Cother_GSSs: RPCI-23-73N16.TV

The Institute for Genomic Research

Fax: 301 838 0208

Fa
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EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACc3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

135 c 112 g 144 t
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/clone="RPCI-11-318M7"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
1 81 c 92 g 177 t
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0;
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-73N16"
/clone="RPCI-23-73N16"
/sex="Fenale"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 CCTTATGATCTGCCTGCCT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 CCTTATGATCTGCCTGCCT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequence.
AZ239913
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A2239913/c
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DEFINITION
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KEYWORDS
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DB 12; Length 545;

1.8%; Score 19;

Query Match

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/note="Vector: Lambda gill Sfi-Not; Site_1: EcoRI; Site_2: NotI: Several hundred adult Schistosoma japonicum(Jiangxi, P.R.China, Strain), of mixed sex, were perfused from the mesenteries of experimentally infected rabbits.

Double-strain cDNA synthesized with the mRNA isolated from adult worm, was inserted into the bacteriophage lambda gill Sfi-Not arms between EcoRI and NotI site of the LacZ gene. The CDNA library was contructed by Chen S.z. at Nanjing Medical University, Nanjing, Jiangsu, P.R. China. (see: Chen Shuzhen, et al. Chinese Journal of zoonoses 1997, 13 (6): 23-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS B1677745 55P pp mRNA linear EST 17-SEP-2001 DEFINITION CLS447 CLS (Cambium and bark region of black locust - Summer)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Parasitology
Sun-Yat-sen University of Medical Sciences
Sun-Yat-sen University of Medical Sciences
Sun-Yat-sen University of Medical Sciences
Fact-sen University of Medical Sciences
Tel: 86-20-87330566
Fax: 86-20-87331679
Email: zdwu62@163.net
                                                                                                                                                                                                                                                                                JAYL0146.GYL Schistosoma japonicum Lambda gtll Express library Schistosoma japonicum cDNA clone JAYL0146.GY 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Schistosoma japonicum Lambda gtll Express
                                         Gaps
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Strigeidida, Schistosomatoidea; Schistosomatidae, Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1. to 554)
Li,Y., Wes. I. to 554)
Li,Y., Wes. I. D. and Yu,X.B.
Expressed sequence tags from adults of Schistosoma japonicum (Chinese strain) (Li,Y.; Wu,Z.D.; Yu,X.B.)
Contact: Wu ZD
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/strain="Chinese"
/db_xref="taxon:6182"
/clone="JAYL0146.0Y"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 19; DB 9; L
100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
              Pred. No. 1.5e+02;
Mismatches 0;
                                                                                                                                                                                                                                                             mRNA
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                                                                                                                                                                                                                                                          554 bp
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                        AW231247.1 GI:6560543
                                                                                                                                                                                                                                                                                                                                                                                                      Schistosoma japonicum. Schistosoma japonicum
                                                                                                                   308 CCTGCCCAGCGTGTCTGCT 290
                                                                                        699 CCTGCCCAGCGTGTCTGCT 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 TCGCCATCATCTATTTG 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Mix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8
Best Local Similarity 100.
Matches 19; Conservative
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BI677745/c
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AW231247
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Mus musculus
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Matches 19; Conserv
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AQ993291/c
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bass 1 to 577)
S. Zhao, S., Nerman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSS: RPCI-23-286kI0.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Site_2: Sfi
n and bark
I in Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPCI-23-286K10.TJ RPCI-23 Mus musculus genomic clone RPCI-23-286K10, DNA sequence. A2041597.1 GI:7134231 GSS.
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                                                                                                Robinia pseudoacacia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Robinieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:35938" //clone_11b="CLS (Cambium and bark region of black locust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="cambial region (Cambium and bark region of black locust - Summer)"
/dev_stage="mature tree"
/note="vector: lambda TiplEx; Site_1: Sfi IA; Site_2: Sf
IB; The cDNA library was made from the cambium and bark region of a mature black locust tree collected in Michiga
                                                                                                                                                                                              1 (bases 1 to 556)
Han, K.-H., Yang, J., Park, S., Paule, C.R., Kapur, V., Retzel, E.F., Kamdem, D.P. and Keathley, D.E.
Analysis of gene expression patterns in trunk wood of a mature black locust (Robinia pseudoacacia)
Unpublished (2002)
Contact: Kyung-Hwan Han
Department of Forestry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                               Michigan State University
126 Natural Resources, East Lansing, MI 48824-1222, USA
Tel: 517 353 4751
Fax: 517 432 1143
Email: hanky@msu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 556;
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1.8%; Score 19; DB 10; 1
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Robinia pseudoacacia"
Robinia pseudoacacia cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .556
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                                     BI677745.1 GI:15630652
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99 c
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                                                                                 Robinia pseudoacacia.
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                ACCESSION
VERSION
KEYWORDS
SOURCE
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A2041597/c
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Onote-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
Cool: Site_2: EcoR: Female C57BL65 mouses kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies).
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Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Email: szhaoétigr.org Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong library availability, please contact Pieter de Jong (pieterédejong.med buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 286 row: K column: 10
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Library avallability, please contact Pieter de Jong
(pieter@dejong.med buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/fdb/Dac_ends/mouse/bac_end_intro.html
Plate: 331 row: E column: 8
Seq primer: T7
Class: BAC ends.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 594)
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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                                                                                                                                                                                                                                                                       Class: BAC ends.
Location/Qualifiers
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GSS.
house mouse.
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source

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1. .594
/organism="Mus musculus"
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ECORI; Site_2: ECORI; Female C57BL/6J mouse Kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
80 a 145 c 113 g 154 t 2 others
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	Œ	AF345568	AL545172	AL546894	BI837965	AL554198	BI820995	BI908162	BM008116	BB873518	BB614132	BB873597	BB849390	BF074336	BI489649	BF230383	BI521556	BB866696
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/tissue_type="location"
//tissue_type="location"
/note="Vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fex: (1) 301 610 8371
Email: //fulllength.invitrogen.com (TR.:
http://fulllength.invitrogen.com (Tr.:
                                                                                                                                                                         870 bp mRNA linear EST 16-FEB-2001
Homo sapiens cDNA clone CSODI028YL20 5
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               AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope_cns.fr, Web : www.genoscope.cns.fr.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (basa 1 to 870)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 801)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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 Length
                                  0; Mismatches 258;
   DB 9;
                    Pred. No. 4.8e-76;
 Score 317.2;
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30.5%;
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Matches 485; Conservative
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/db_xref="taxon:9606"
/dl_xref="taxon:9606"
/clone_"CSDIO1267P01"
/clone_lib="LTI_NELO6_PL2"
/tissue_type="placenta"
/note="vector: pcWNSPORT 6; Site_l: Not!; lst strand cDNA was primed with a Not!-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL546894 LTI_NFL006_PL2 Homo saplens cDNA clone CSODIO26rP01 5 prime, mRNA sequence.
AL546894 GI:12880455 EST. Sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
                    569 GGTGCAAATTTGTGCAGCAGCTTCAGCATCTGCCATACCTTCCAGTGGCACGAAGCCATG
                                                                                                                                                                                                                                                                  TICCAGCIGGAGIICIIIAAGCCCCTCGGCAICAICITAITITGCICCIICAAGAIIGII
   GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
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                                                                 CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTTGCACCCTGTGG
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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TGGGCTTTTGGGÅCATTCCTGCCGAGTGGGGTTTCACGTTGGCCATGAACAGGGCC 300
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Email: segref
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| J. 801
| John | John
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             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM11560 row: b column: 01
High quality sequence stop: 796.
Location/Qualifiers
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Pred. No. 8.2e-74;
0; Mismatches 240; Indels
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/done_lib="CSDAION31808"
/clone_lib="LTI_NFL006_PL2"
/clone_lib="LTI_NFL006_PL2"
/clone_lib="LTI_NFL006_PL2"
/clone_lib="LTI_NFL006_PL2"
/clone_lib="LTI_NFL006_PL2"
/clone_lib="Vector: pCMVSPORT 6; Site_l: NotI; ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enfined, double-strands cDNA was digested with Not I and enfined; outle strands cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 8000 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Emdil: filangthiletech.com URL : http://tullength.invitrogen.com"
ttp://tullength.invitrogen.com"
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                                                                                                                                                                                                                                                                                                                                                         855 bp mRNA linear EST 16-FEB-2001
NFL006_PL2 Homo sapiens cDNA clone CSODI081YK03 5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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637 TICCICCIGGAGIIGIICCIGCCCCIGGGCAICAICCIGIICIGCICAGCCAGAAIIAIC 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Centre National de Sequencage
EVRY cedex - France
fågenoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                  GTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG
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                                                                                                                                                            Juber, C., Jessee, J. and Polayes, D. CDNA libraries and normalization (2001)
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/db_xref="taxon:9606"
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bp mRNA linear EST 16-OCT-2001 sapiens cDNA clone IMAGE:5216512 5',
male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by 6 Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MCC Library."
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                                                                                                                                                                                                                                                                             91 ATAGACAAGAAGAACTGCTGTGTGTTCCGAGATGACTTCATTGTCAAGGTGTTGCCGCCG 150
                                                                                                                                                                                                                                                                                                               61 CTGCTCATTGTGGCCTTTGTGCTGGCGCCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
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                                                                                                                                                                                                            0; Mismatches 249;
                                                                                                                                                                          Score 278.6; DB 1
Pred. No. 1.9e-65;
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                                                                                                                                                                        Query Match 26.8%;
Best Local Similarity 64.6%;
Matches 463; Conservative
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mRNA sequence.
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pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp mRNA linear EST 04-OCT-2001
sapiens cDNA clone IMAGE:5176597 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mather Lipter; //mgc.nci.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Geomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Htp://lmge.llnl.gov

Plate: LLAMI1440 row: a column: 14

High quality sequence stor: 6

High quality sequence stor: 6

Location/Qualifiers
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                                                                                                                                                                        421 GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG 480
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 331 TGGAAGTTTGGGGACATCCCTTGCCGGCTGATGCTCTTCATGTTGGCTATGAACCGCCAA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAGCCTGAGGCGGAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                  691 TKGAGCCTGCGGCAGAG---ACAAATGGACCGGCATGCCAAGATCAAGAGAGCCAACACC
                                  CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCTGTGG
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/clone="IMAGE:5176597"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_cxref="taxon:9606"
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/clone='Inb=NIH_WCC_118"
/tissue_type="leukocyte"
/tissue_type="leukocyte"
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/note="vector: pCWV-SPORT6; Site_1: Not1; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC_Library."
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                                                                                   L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11543 row: p column: 17
High quality sequence stop: 731.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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0; Mismatches 211; Indels
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/clone_lib="NHH_MCC_lis"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-DNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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603618002F1 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:5450832 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1940 row: d column: 01
High quality sequence stop: 752.
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564 ACTGCAAATGTGTGCATCAGCTTCAGCATCTGCCATACCTTCCGGTGGCACGAAGCTATG
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Pred. No. 2.4e-62;
0; Mismatches 213; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:5450832"
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Bummalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 660)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
                                                                                                         FIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1771-1771 (2000) (11), 1771-1771 (2000) (11), 1771-1771 (2000) (11), 1771-1771 (2000) (11), 1771-1771 (2000) (11), 1771-1771 (2000) (11), 1771-1771 (2000) (11), 1771-1771 (2000) (11), 1771-1771 (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2
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               Ozawa, K., Tanaka, T., Matsuura
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/clone="c630046N17"
/clone_lib="RIKEN full-length enriched, 15 days embryo brain"
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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/organism="Mus musculus"
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BB873518.1 GI:17119728
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URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konnoh., Okazaki,Y., Muramatsu,M. and Hayahzaki,Y.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 367)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishli, Y., Tto, M., Kawal, J., Kolima, M., Matsuyama, T., Y., Tto, M., Matsuyama, T., Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Tayashashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Towari, K., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
Unpublished (2001)
Unpublished (2001)
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (BIKEN)
Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-resigns.riken.go.jp,

UR.:http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa libraries for rappid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I."
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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head"
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Pred. No. 6.5e-59;
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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Location/Qualifiers
1. .660
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="4833417H22"
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazak,Y.', Hayatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanaka,T., Matsuura
'S., Kawai,J.', Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
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             The Institute of Physical and Chemical Research (RIKEN)
17-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
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Pred. No. 1.2e-58;
0; Mismatches 58; Indels
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/dev_stage="15 days embryo"
106 c 92 g 104 t
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/organism="Mus musculus"
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Best Local Similarity 83.2%;
Matches 288; Conservative
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Sciences Center(GSC), Yokohama Institute
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URL:http://genome-gscriken.go.jp,
URL:http://genome-gscriken.go.jp,
URL:http://genome.gscriken.go.jp,
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URL:http://genome.gscriken.go.jp,
Wormalization and subtraction of Cap-trapper-selected cDNnsk
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake.S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Osawa, K., Tanaka, T., Matsuura
S., S., Rawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y., Barkai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 110 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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/clone="F930010D18"
/clone_lib="RIKEN full-length enriched, adult inner ear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 3e-52;
0; Mismatches 90; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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109 c 119 q
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BB849390.1 GI:17090844
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Best Local Similarity 77.5%;
Matches 330; Conservative (
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us-09-886-041-1.std.rst

Duery Match  21.0%; Score 218.2; DB 10; Length 550; Best Local Similarity 68.6%; Pred. No. 5.9e-49; Matches 301; Conservative 0; Mismatches 138; Indels 0; Gaps 0; 16 TGCTGCCGCACCACCATCCCCAGGTGATGCCGCCGCTGCTGTGGCC 75 16	3 5-5 8-8 6 5 g	I (Mases I I (Mases I I (Mases I I (Mathematical I I (Mathematical I I I I I I I I I I I I I I I I I I I
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09 312 GTTCCTTACGGTGGTGGCGGACAGGTATTCAAAGTGGTCCACCCCCACCAGGGGG 371  121 CTTCCTCACTGGTGGTGGTGGTATTCAAAGTGGTCCACCCCCACCAGTGT 180  09 372 GAACATTCTCCACTGGTGGCTGGCTGGTTTCAAGTGGTCCACCCCCACTATGGT 180  09 432 CAGGACTATCTCCACCGGTGGCTGGCTGGTCTCTGGTTCAT 240  09 432 CCTGGGAACATTTTGTGGTGGAACCATCTTTGGTGCACTTTGTTCT 491  1	RESULT 13  BF074336  BF074336  BF074336  DEFINITION  221723 MARC 2BOV BOS taurus CDNA 5', mRNA sequence.  ACCESSION  BF074336.1 GI:10867847  REYNORDS  COW.  ORGANISM  BEO74336.1 GI:10867847  SOURCE  ORGANISM  BEO74336.1 GI:10867847  COW.  ORGANISM  BEO74336.1 GI:10867847  COM.  ORGANISM  BF074336.1 GI:10867847  COM.  ORGANISM  BF074336.1 GI:10867847  COM.  BF074336.1 GI:10867847  COM.  COM.  BF074336.1 GI:10867847  COM.  COM.  BF074336.1 GI:10867847  COM.  BF07436.1 GI:10867847  COM.  CO	Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR PRIMERS FORWARD: AGGAAACAGCTATCACCAT BACKWARD: GTTTTCCCAGTCACGACG Plate: 80 row: K column: 23 Seq primer: ATTAGGTGACACTATAG. Location/Qualifiers source //Organism="Bos taurus" //Ob_rref="taxon:9913" //lone="taxon:9913" //lone="taxon:9913" //lab_host="minol" //lab_host="pooled" //lab_host="poo

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/note-"Organ: pooled brain, lung, testis; Vector:
pcMV-SPORT6; Site_1: NotI: Site_2: EcoRV (destroyed); RNA
source annonymous pool of 6 male brains, age fange 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
estroyed upon cloning). Average insert size 18 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: tis is an HL MC Library."
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Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S.
                                                                                                                                                                                                                                                                                                              TCCCAGGTGATGCCGCCGCTGTTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGG
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                                                                                                                                                                                                                                          Length 636;
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Pred. No. 2.9e-48;
0; Mismatches 177; Indels
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Best Local Similarity 64.5%;
Matches 322; Conservative
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SOURCE
ORGANISM
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ORIGIN
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COMMENT

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/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease
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USDA, ARS, Beltsville Agricultural Research Center Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA Pel: 301 504 8416 Fax: 301 504 8414 Email: tads@lpsi.barc.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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Pred. No. 9.4e-48;
0; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                       134
                                                                                                                                                                                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_llb="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Job time : 1736 secs
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Matches 290; Conservative
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Sequence 62, Sequence 62, Sequence 62, Sequence 62, Sequence 63, Sequence 9, A Sequence 1, A Sequenc

Sequence Sequence Sequence

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GENERAL INFORMATION:
APPLICANT: Hadcock Dr., John R.
APPLICANT: Ozenberger Dr., Bradley A.
APPLICANT: PRUSCH Dr., Mark H.
TITLE OF INVENTION: Receptor Identification Method
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: American Home Products Corporation STREET: One Campus Drive CITY: Parsippany STATE: New Jersey COUNTRY: USA
                                                   US-07-816-283-3
US-08-417-103-3
US-08-417-103-3
US-08-417-840-62
US-08-476-976-62
US-08-476-976-62
US-08-410-62
US-08-486-673-9
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ORGANISM: Rat
PUBLICATION INFORMATION:
AUTHORS: Hadcock Dr., John R.
AUTHORS: Dr. Ozenberger, Bradley A.
AUTHORS: Dr. Pausch, Mark H.
TILLE: Receptor Identification Method
DATE: 17-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/915,966C
FILING DATE: 17-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale M.
REGISTRATION NUMBER: 31,829-00
REFERENCE/DOCKET NUMBER: 31,829-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2134
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTREISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/07915966C Patent No. 5668006
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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STATE: NE
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Sequence 43,
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Sequence 11,
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-771-182-1

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US-08-133-194-1

US-09-130-749-1

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US-08-144-581B-1

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US-08-476-976-3
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Database :

Result

Searched:

Sequence:

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                         Length 545;
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Fatent No. 5929209
GENERAL INFORMATION:
APPLICANT: Ozenberger Dr., Bradley A.
APPLICANT: Pausch Dr., Mark H.
TITLE OF INVENTION: Receptor Identification Method
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ANDRESS:
ADDRESSEE: American Home Products Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,182 FILING DATE: 20-DEC-1996 CLASSIFICATION: 435
                        Score 229.6; DB 1;
Pred. No. 4.5e-57;
0; Mismatches 189;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         22.1%;
65.0%;
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                        Query Match 22.1
Best Local Similarity 65.0
Matches 356; Conservative
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CITY: Parsippany
STATE: New Jersey
COUNTR: NSA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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157 TACCTITICAATTIGGCCGTGGCTGATITCCTCCTTATGATCTGCCTGCCTTTTCGGACA 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 GAGAACCATCTCTGCGTGCAAGAGACGGCCGTCTCTGTGAGAGCTTCATCATGGAGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 GTCAAGATCAAGAGGCCCATCAATCATCATGATGGTGGTTGCCATTGTGTTTGCCATTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 TICACGIIGGCCAIGAACAGGGCCGGGAGCAICGIGTICCIIACGGIGGIGGCIGCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AGGTACTTCAGGGTGGTCCACCCGCACCACTTCCTGAACAAGATCTCCAACCGGACGGCG
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Pred. No. 4.5e-57;
0; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Dr. Ozenberger, Bradley A. AUTHORS: Dr. Pausch, Mark H. TITLE: Receptor Identification Method DATE: 20-DEC-1996
                                                      REFERENCE/DOCKET NUMBER: 31,81
REFERENCE/DOCKET NUMBER: 31,81
TELECOMMUNICATION INFORMATION:
TELERAX: 201.683-4117
TELERAX: 201.683-4117
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
TYRE: nucleic acid
STRANBEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Hadcock Dr., John R. AUTHORS: Dr. Ozenberger, Brad
                                            32,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.1%;
Best Local Similarity 65.0%;
Matches 356; Conservative
ATTORNEY/AGENT INFORMATION:
                   NAME: Matthews, Gale F. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Rat
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-CENT
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421 CTGTTCTGCTCTGGCAGGATCATTTGAGCCTAAGGCAGAG---ACAGATGGACAGGCAC 477
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                              397 GCTGGCATCGTCTGCACCCTGTGGGCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTG 456
                                                                                    241 GCCATCATCTTGCTTGCTGTGGGGCATCACCATCGGCCTGACAGTCCACCTCCTCAC
                                                                                                                                              GAGAACCATCTCTGCGTGCAAGAGACGGCCGTCTCCTGTGAGAGCTTCATCATGGAGTCG
                                                                                                                                                                                                                                                                                                                                                                                     577 ITATTTTGCTCCTTCAAGATTGTTTGGAGCCTGAGGCGGAGGCAGCAGCTGGCCAGCAG
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Patent.No. 5955308
GENERAL INFORMATION:
APPLICANT: MOONEY, JEFFREY
APPLICANT: MOONEY, JEFFREY
APPLICANT: HALSEY, WENDY
TITLE OF INVATION: CDNA CLONE HEOAD54 THAT ENCODES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: RATNER & PRESTIA
T: P.O. BOX 980
VALLEY FORGE
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: DISKette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOPPERATING SYSTEM: DOS
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STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
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STRANDEDNESS: single
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US-08-955-713-1
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                                                GENERAL INFORMATION:
APPLICANT: Hadcock Dr., John R.
APPLICANT: Ozenberger Dr., Bradley A.
APPLICANT: PRUSCH Dr., Mark H.
TITLE OF INVENTION: Receptor Identification Method
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                     COUNTER: United States of America
ZIP: 06904-0060
ZIP: 06904-0060
COMPUTER REDABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/853,194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.1%; Score 229.6; DB 3; Best Local Similarity 65.0%; Pred. No. 4.5e-57; Matches 356; Conservative 0; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Hadcock Dr., John R.
AUTHORS: Dr. Ozenberger, Bradley A.
AUTHORS: Dr. Pausch, Mark
ITLE: Receptor Identification Method
BATE: 17-JUL-1992
US-08-853-194-1
                                                                                                                                                                                                           STREET: One Cyanamid Company STREET: One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/915,966
FILING DATE: 17-JUL-1992
ATTORNEY AGENT INFORMATION:
NAME: TSEVGOS Dr., EStelle J.
REGISTRATION NUMBER: 31,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31829-00
Sequence 1, Application US/08853194
Patent No. 6077666
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TELERAX: 203-321-2.
TELERX: 710-474-4059
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
"YPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
TELEFAX: 203-321-2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Rat
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTT-CENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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53 TGCCGCCGCTGCTCATTGTGGCCTTTGTGCTGGCGCCACTAGGCAATGGGGTCGCCTGT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGTGGCTGATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 GTAGACACTGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 ATGAGACCTGGCGCTTTGGGGCTGCTGCCTGCAAAGTCAACCTCTTCATGCTGTCNACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 TCCACCCCCACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 CCCTGTGGGCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGGGCCGGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/08/955,713

FILING DATE: 23-007-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/050,124

FILING DATE: 18-JUN-1997

ATTORNEY AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTATION NUMBER: 23.031

REFERENCE/DOCKET NUMBER: GH-70087

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
      ADDRESSEE: RAINER & PRESTIA STREET: P.O. BOX 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1435 base pairs TYPE: nucleic acid
                                                                                                                                                          IBM Compatible
                                                                                                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                      STREET: P.O. BOX 9 CITY: VALLEY FORGE
                                                                                                                                                            COMPUTER: IBM COI
OPERATING SYSTEM:
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                                                                                   USA
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                                                                                 COUNTRY:
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                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1173 TCTTTGGCATGGCTTCCATGGTGGCTTTCTGGCTGTCCGCCTGCCGCTCCTTGGACCTCT 1232
                                                                                                                                                                                                                                                                                                                                                                                                                       412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATCATGTTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCA 592
                                                                                                   GIGGITICIGCITCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 CCCTGTGGGCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCG 472
                                                                             TGCCGCCGCTGCTCATTGTGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGT 112
                                                                                                                                                                                                                                                                                                                                                        599 ATGAGACCTGGCGCTTTTGGGGCTGCTGCTGCAAAGTCAACCTCTTCATGCTGTCCACCA 758
                                                                                                                                                                                                                                       CCGTGGCTGATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGAC
                                                                                                                                                                                                                                                               579 TCATCTTCTGCATCCACACGCGCCCTGGACCTCCAACACGGTGTTCCTGGTCAGCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                               293 ACAGGGCCGGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGGCAGGTATTTCAAAGTGG
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                                            12;
      Length 1594;
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Patent No. 5955308
GENERAL INFORMATION:
APPLICANT: AZTHE, GANESH
APPLICANT: MOONEY, JEFFREY
APPLICANT: HALSEY, WENDY
TITLE OF INVENTION: CDNA CLONE HEOAD54 THAT ENCODES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
  Score 188.8; DB 2;
Pred. No. 4.9e-45;
); Mismatches 357;
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Similarity 54.7%;
5; Conservative (
                                        445;
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.08-955-713-3
      Query Match
                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
                      62 TGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTCT 121
                                                                                                                                     299 TGGGGATGGCCTTCCTGGCCGCGTGGCTTTGGACCGGTACCTCCGTGTGGTCCACCCTC
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                                                                                                            122 GCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCTG
                                                                                                                                                                                                  182 ATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACACT
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                                                                                                                                                                                                                                           179 ACCTGCTGTTGGCTGCCTGCCTTTCCTGGCCGCCTTCTACCTGAGCCTCCAGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SHABON, USMAN
APPLICANT: SHABON, USMAN
APPLICANT: ELSHOURBAGY, NABIL
TITLE OF INVENTION: MCLECULAR CLONING OF A 7TM
TITLE OF INVENTION: RECEPTOR (GPR31A)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATMER & PRESTIA
STREET: P.O. Box 980
CITY. VALIEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09130749 Patent No. 6031344 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 495 AGGCACTGTACCTGCTGGARTTYTTCCTGCCACTGGCGCTCATCCTCTTT---GCTATTG 551
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                                           593 AGATTGTTTGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAGG
                                                                                                                                                                                                                                                                                                         773 GGGCCCTGCACATAA-----CCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCC
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MEDIUM TYPE: DISKette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,749
FILING DATE: 07-Aug-1998
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A 7TM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: «Unknown>
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELSHOURBAGY, NABIL TITLE OF INVENTION: MOLECULAR CLONING OF
                                                                                                                                                                                                                                                                                                                                                                                            827 TGGTGTATTTTTCAAGCCCCTCCTTTCCCAA 860
                                                                                                                                                                                                                                                                                                                                                                                                                     792 TGCTCTACTGCTTCTAGCCCCAACTTCCTCCA 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: RATWER & PRESTIA
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09130749
Patent No. 6031090
GENERAL INFORMATION:
APPLICANT: SHABON, USMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 610-407-0701
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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JLE TYPE: cDNA
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US-09-130-749-1
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599 TCATCAGGGCTCTCCAGAAAAGACTCCGGGAGCCTGAGAAACAGCCCCAAGCTTCAGCGGG 658
                                                                                                                            713 CTGCTAGACT-CTATTTCCTCTGGACGGTGCCTCGAGTGCCTGCGATCCCTCTGTCCAT 771
                                                                                                                                                                   719 TGGCCAGAGTCCTGATGCACATCTTCCAGAATCTGGGGAGCTGCAGGGCCCTTTGTGCAG 778
                                                                                                                                                                                                            772 GGGGCCCT----GCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCC 826
                                           653 CGACCCGGTTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                               827 IGGIGIATIATITICAAGCCCCTCCTITCCCAAAITCTACAACAAGCIC 876
                                                                                                                                                                                                                                                                                                                       6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 47,18
Matches 377; Conservative
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701..1717
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STATE: Illinois
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; LOCATION:
US-08-153-848-43
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US-08-153-848-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 ATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACGAGTTATTACCTCAGACGTAGACACT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 GECATCTGGGCCGGGTGCTGGGCCCTGCGCTTCCTGGACCTCAGCCGCAGCG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 139.2; DB 3; Length 960;
Pred. No. 8.6e-31;
0; Mismatches 388; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 GGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 GGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 CCCTGGTCATCCTGGGAACAGTGTATCTTTGCTGGAGAACCATCTCTGCGTGCAAGAGA
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                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GP-70513
TELECOMUNISTATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                            UMBER: US/09/130,749
07-AUG-1998
                                                                                                                                                                                                                                                                                                                                        23,031
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Best Local Similarity 51.4%;
Matches 427; Conservative
                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,0
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 846169
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                              APPLICATION NUMBER:
FILING DATE: 07-AUG
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
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Best Local Similarity
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TOPOLOGY:
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                                                                                                                                                                                                                  288 CATGAACAGGGCCGGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648 GAAGGCGACCCGGTTCATCATGGTGGTGGCAATTGT-----GTTCATCACATGCTA 698
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                            855
                                                                                                                                                               CAGACGTAGACACTGGGGTTTTGGGGACATTCCCTGCCGAGTGGGGGCTCTTCACGTTGGC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               588 CTTCAAGATTGTTTGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAA 647
                                                   108 CCTGTGTGGTTTCTGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAA 167
                                                                                                        48 GGTGATGCCGCCGCTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGC 107
               CTGCGTGCAAGAGGCCGTCTCTGTGAGAGCTTCATCATGGAGTCGGCCAATGGCTG
                                                                                                                                                                                                                                                                       348 AGTGGTCCACCCCCACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGT
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APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TILE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Borun
6300 Sears Tower, 233 South Wacker Drive
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STATE: Illinois
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1096 CATTGTGCACCCGGTCAAGTCCCTCAAGCTCCGCAGGCCCCTCTACGCACACCTGGCCTG 1155
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COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PLLICATION NUMBER: US/09/299,843A PTLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109; DB 3; L
Pred. No. 6.6e-22;
0; Mismatches 415;
                                                                                                                                                                                                                                    PELCRATION 433
PRIOR APPLICATION 433
PRIOR APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTONREY/AGNIT INFORMATION:
NAME: Jil E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFRAX: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 377; Conservative
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: linear
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1216 CGTGCAGACCACACGGTGGTCTGCCTGCAGCTGTACCGGGAGAAGGCCTCCCACCA 1275
                                                                                                                                    1516 GCGCATCCTGGCCCTGGCAACCGCATCACCTCCTCCTCCTCACCAGCCTCAACGGGGCACT 1575
                                                                                 1276 TGCCCTGGTGTCCCTGGCAGTGGCCTTCACCTTCCCGTTCATCACCACGGTCACCTGCTA 1335
                                                                                                                                                                                                                                                     CCTGCCCAGCGTGTCTGCTAGACTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                 588 CTTCAAGATTGTTTGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAA
                                                                                                                                                                                   648 GAAGGCGACCCGGTTCATCATGTGGTGGCAATTGT-----GTTCATCATGCTA
                                                                                                                                                                                                                                                                                    1456 GETCAACCGCTCCGTCTACGTGCTGCACTACCGCAGCCATGGGGCCTCCTGCGCCCCCA
                                                528 GCATGACATCATGTTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATGTTTTGCTC
                                                                                                                                                                                                                                                                                                                       759 TCCCTCTGTCCATGGGGCCCTGCACATAACCCTCAGCTTCACCTGCATGAACAGCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Palent In PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURENT APPLICATION DATA:

APPLICATION NOWBER: US/09/088,337B

FILING DATE: 01-Jun-1998

CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION NOWBER: US 08/153,848

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

RELIGNO DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

RESISTRATION NUMBER: 30022

ATTORNEY/AGENT INFORMATION:

RESISTRATION NUMBER: 30022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09088337B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (312) 474-0448
TELEX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                         819 GGATCCCCTGGTGTATTT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 43:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Applicati
Patent No. 6348574
GENERAL INFORMATION:
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1216 CGTGCAGACCACCACGACGTGGTCTGCAGCTGTACCGGGAGAAGGCCTCCCACCA 1275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1456 CGTCAACCGCTCTACGTGCTGCACTACCGCAGCGATGGGGCCTCCTGCGCCACCCA 1515
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                                                                                                                                                                                                                                                                                                                                                                                                               108 CCTGTGTGGTTTCTGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     856 TCTGTGGCTTTTCATCCGAGACCACAGTCCGGGACCCCGGCCAACGTGTTCCTGATGCA 915
                                                                                                                                                                                                                                                                                                        GGTGATGCCGCCGCCGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGC 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468 CTGCGTGCAAGAGGCCGTCTCCTGTGAGAGCTTCATCATGGAGTCGGCCAATGGCTG
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                                                                                                                                                                                               Length 1901;
                                                                                                                                                                                         Score 109; DB 4; Length 19
Pred. No. 6.6e-22;
0; Mismatches 415; Indels
                                                         LOCATION: 701..1717
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-088-337B-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 43, Application PC/TUS9311153 ; GENERAL INFORMATION:
  DNA (genomic)
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                                                                                                                                                                                         10.5%;
ilarity 47.1%;
Conservative
                                                      NAME/KEY:
MOLECULE TYPE:
                                                                                                                                                                                                                         Similarity
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1276 TGCCCTGGTCCCTGGCAGTGGCCTTCACCGTTCATCATCACCACGGTCACCTGCTA 1335
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    408 CTGCACCCTGTGGGCCCTGGTCATCTGGGGAACAGTGTATCTTTTGCTGGAGAACCATCT 467
                                                                                                                                                                   528 GCATGACATCATGTTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTC 587
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                                                                                                                                                                                                                                                                                                                                 648 GAAGGCGACCCGGTTCATCATGGTGGTGGTGCAATTGT-----GTTCATCATCATGCTA
                                                                                     CTGCGTGCAAGAGACGGCCGTCTCCTGTGAGAGCTTCATCATGGAGTCGGCCAATGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                               699 CCTGCCCAGCGTGTCTGCTAGACTCTATTTCCTCGGACGGTGCCCTCGAGTGCCTGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LI, YI
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: GOCAYNE, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN, CECCHI,
ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NJ
COUNTRY: NJ
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application PC/TUS9507180 GENERAL INFORMATION:
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NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               819 GGATCCCCTGGTGTATTT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 2453 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 CATGAACAGGGCCGGGAGCATCGTGCTTACGGTGGTGGCTGCGGACAGGTATTTCAA 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 GGTGATGCCGCCGCTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGC 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 TITGCCCGTGCTGATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCT 227
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Pred. No. 6.6e-22;
0; Mismatches 415; Indels
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vickl L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
                                                                                                                  STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/US93/11153
                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 47.1%;
Matches 377; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 701..1717
PCT-US93-11153-43
                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                           COUNTRY:
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421 TCTATGTTACCGTGCTGGTGGTGGCTTCCCGGCCAACTGCCTGTCCCTCTACTTCGGCT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 GCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 CCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAGA 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 ACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGGG
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                                                                                                                                                                                                STORAGE
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Pred. No. 1.5e-20;
0; Mismatches 443;
                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKilne Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
                                                                                                                                                           2IP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
COMPUTER: IBM 486
                                                                                                                                                                                                                                       OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
                                                                                                                                                                                                                                                       SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,974A
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATG50022
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REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610_270_5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.0%;
Best Local Similarity 46.9%;
Matches 399; Conservative (
HUVCT36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acid
EDNESS: Single
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linear
                      NUMBER OF SEQUENCES
                                                                                                                STATE: PA
COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: Line
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-724-974A-1
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A No. 5912335el G-Protein Coupled Receptor
                                                                                                  Length 2453
                                                                                              Score 109; DB 5; Length 24
Pred. No. 7.5e-22;
0; Mismatches 415; Indels
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APPLICANT: Derk J. Bergsma, Cathe TITLE OF INVENTION: A No. 5912335
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                                                                                              Query Match
Best Local Similarity 47.1%;
Matches 377; Conservative
                    CDS
548..1564
                    NAME/KEY:
                                      ; LOCATION:
PCT-US95-07180-1
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596 TTGTTTGGAGCCTGAGGCGGGGGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGA
                                  841 ACCAGCACCGCGTGTGCTTTGAGCACTACCCCATCCAGGCATGGCAGCGCGCCATCAACT
                                                                       536 TCATGITCCAGCTGCAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGA
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APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
TITLE OF INVENTION: Null Cells Expressing P2U Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Bell, Seltzer, Park & Glbson STREET: Post Office Drawer 34009 CITY: Charlotte STATE: No. 5596088th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/442,134A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08442134A Patent No. 5596088 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weisman, Gary A.
Turner, John T.
Harden, Thomas K.
Parr, Claude E.
Sullivan, Daniel M.
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SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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APPLICANT: Harden, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Sullivan, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
TITLE OF INVENTION: Null Cells Expressing P2U Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 Length 1842;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                       0; Mismatches 204;
                                                                                                                                                              8.9%; Score 92.6; DB 1; 51.3%; Pred. No. 3.6e-17;
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APPLICATION NUMBER: US/08/444,581B
FILING DATE: 19-MAY-1995
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Weisman, Gary A.
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Matches 215; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                               57..1181
MOLECULE TYPE: CDNA FEATURE:
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                                                     NAME/KEY:
LOCATION:
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APPLICANT:
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Pred. No. 3.6e-17;
0; Mismatches 204; Indels 0
                                          ALECOMOUNICATION

REGISTRATION NUMBER: 31,665

REGISTRATION NUMBER: 5470-71A

REFERENCE/CONCET NUMBER: 5470-71A

TELEPHONE: 919-420-2200

TELEPHONE: 919-811-3175

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 11near
US 08/442,134
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 51.3%;
Matches 215; Conservative (
            FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER:
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57..1181
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; LOCATION:
US-08-444-581B-1
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: sp_archea:*
2: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPTREMBL_19:*
                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                 Sedneuce:
                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*

sp\_plant:\*

sb\_phage: \*

4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_manmal:\*
7: sp\_mhc:\*
8: sp\_organelle:\*

sp\_fung1:\*

## SUMMARTES

					SUMMAKIES	
		æ				
Result No.	Score	Query Match	Duery Match Length DB	DB	QI	Description
1	1853	100.0	346	4	09BXC0	neines omod Obxdo
7	868.5	46.9	360	. =	098566	ninskim skim ggaego.
က	450.5	24.3	319	4	09NO20	Ogna20 homo sapien
4	446.5	24.1	319	11	09JLS1	0911s1 mus musculu
S	371.5	20.0	309	11	0920A1	0920al mus musculu
9	366.5	19.8	330	4	09нс02	Oghca2 homo sapien
7	366.5	19.8	346	4	09NS75	Ogns75 homo sapien
60	362	19.5	345	9	Q95N03	095n03 sus scrofa
6	355.5	19.2	309	11	0924T9	0924t9 rattus norv
10	342.5	18.5	357	13	Q9DE05	09de05 rafa erinac
11	341	18.4	361	13	090X57	090x57 xenopus lae
12	336	18.1	367	4	Q9UE21	Ogue21 homo sapien
13	334	18.0	298	4	920n60	Ogudz6 homo sapien
14	329.5	17.8	380	13	909060	Ogdade carassius a
15	317	17.1	373	11	09CPZ4	Ogcoz4 mus musculu
16	310	16.7	377	4	096ЕМ8	Q96em8 homo sapien

095n02 sus scrofa 097271 homo sapien 091010 ovis aries 096ge0 homo sapien 096ff2 homo sapien 095k86 ovis aries 091y73 mus musculu 07667 homo sapien 096ff10 homo sapien 099kp7 sus scrofa 09746 musleagris g 09746 musleagris g 09746 musleagris g 099mt6 mus musculu 099mt6 mus musculu 096p8 bos taurus 099mt6 mus musculu 096p1 an troglod 096p8 homo sapien 096p8 homo sapien 099mt7 mus musculu	0911y8 rattus norv 09by21 homo saplen 0924t8 rattus norv 09byx5 homo saplen 0964d4 periplaneta 091171 mus musculu
6 095N02 4 091C0 6 09N011 4 096GE0 6 095K56 11 091X73 4 076K17 6 095K17 6 095K17 11 095K14 6 04668 11 095K14 6 04668 11 095K14 11 099W17 11 099W17	11 09JLY8 4 09BY21 11 09BY21 4 09BYX5 5 0964D4 11 09JJ71
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,	355 355 355 335 335 335 335
	15.5 15.5 15.5 15.5 4
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	288 287.5 286.5 286.5 286.5 285.5
	4444 4443 4443 45443

## ALIGNMENTS

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RESULT 1

OBENCO

DAG

OBENCO

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OBENCO

DEBLIMINARY;

PRT; 346 AA.

OBENCO

OBENCO
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100.0%; Score 1853; DB 4; Length 346;

Query Match

241

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66 CLPFLAAFYLSLQAWHLGRVGCWALHFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 OLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CSAPSTVVATAVGVLLGLECGLGLIGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                        242 YELWTVPS---SACD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 LSPQAALGVSGLVWLLMVALTCPGLLISE -- AAQNSTRCHSF - YSRADGSFSIIWQEALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMF
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Almeida J.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AL121935; CAB99329.1;
INTERPTO; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPRCHDODPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 AA; 35074 MW; 2ACD0350AD7FB53A CRC64;
                                                                                                                                                                                                                                                                                                                           01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2001 (TrEMBLrel. 17, Last annotation update)
BASI7H2.2 (G PROTEIN-COUPLED RECEPTOR 31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.3%; Score 450.5; DB 4; larity 34.4%; Pred. No. 6e-37; Conservative 61; Mismatches 121;
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                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                               LKPKQPGHSKTQRPEEMPIS 316
                                                                                                                                                                                                                             310 LRKKTLGEPDNNRSTSVELT 329
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Matches 101;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q9JLS1;
               122
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Q9JLS1
ID Q9JLS
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                                                                                                                        HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                                                                                                                                                                                  FOLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                                                                                                                                                                                                                                            DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                                                                                                                                                                                                                                                                                          LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
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                                                             NG-SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVAD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-129/SVJ, AND C57BL/6;
Schaub A., Futterer A., Pfeffer K.;
Schaub A., Futterer A., Pfeffer K.;
PUMA-G, an interferon-gamma inducible gene in macrophages is a nove member of the seven transmembrane spanning superfamily.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJ300199; CAC17791.1;
--- SIMILARITY: BLONGS TO FAMILY 1.--
EMBL; AJ300199; CAC17791.1;
--- SIMILARITY: BELONGS TO FAMILY 1.--
HSSP: P34996; 1DDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.9%; Score 868.5; DB 11; Length
55.6%; Pred. No. 9.3e-79;
.ive 39; Mismatches 96; Indels
                 Indels
                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1933333; Pumag.
InterPro; IPR000276; GPCR_Rhodpsn.
PROMO1; 7tm_1; 1.
PROSTTE; PRO0237; GPCRRHODDPSN.
PROSTTE; PS00237; G_PROTEIN_RECEP_FI_1; 1.
PROSTTE; PS00217; G_PROTEIN_RECEP_FI_2; 1.
SEQUENCE 360 AA; 41400 MW; CCCE52A247577FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE SEVEN TRANSMEMBRANE SPANNING RECEPTOR.
PUMAG OR PUMA-G.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
 Pred. No. 2.2e-177;
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              Mismatches
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              ó
100.08;
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Matches 178; Conservative
              Matches 346; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
Best Local Similarity
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Q9EP66;
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SEQUENCE
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09HCQ2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 -- LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 ISTRVAAGIVCTLWALVILGTVYLLLENHLC-VQETAVSCESFI----MESANGWHDIMF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CSAASTVVETAVGTMLTLECVLGLMGNAVALWTFFYRLKVWKPYAVYLFNLVVADLLLAT 65
                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                         monse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hul Y., Funk C.D.; Molecular cloning of the murine cysteinyl leukotriene type
                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.1%; Score 446.5; DB 11; Length 32.5%; Pred. No. 1.5e-36; ive 64; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Schimenti J.C.; "ORFless, intronless, and mutant transcription units in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 319 AA; 35551 MW; 571F6DFB485BD7C4 CRC64;
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01-DEC-2001 (TTEMBLrel. 19, Last sequence update)
01-DEC-2001 (TTEMBLrel. 19, Last annotation update)
07-STELNYL LEUKOTRIENE RECEPTOR TYPE 2.
CYSLEL
                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           complex responder (Tcr) locus.";
Mamm. Genome 10:869-976(1999).
Mambl., AF14/008; AR726668.1; -.
MGD: MGI:9843; Tcp10c.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR000237; GPCRRHODOPSN.
PROSITE; PS500237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
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01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, G PROTEIN COUPLED RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 104; Conservative
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69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 ADFILMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 PHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHICVQETAVSC---ESFIMESANGW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 VADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 NGWHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFIT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                             3 NGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLAV 59
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Homo sapiens cysteinyl leukotriene receptor 1 like receptor."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB04164; BAB16379.1; -.
InterPro: IPR000275; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                   DB 11; Length
                                                                                                                                                 20.0%; Score 371.5; DB 11; Length 32.7%; Pred. No. 4.7e-29; ive 56; Mismatches 125; Indels
receptor, Cyslt2.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF331658; AAK97354.1; -.
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                                                                                                  309 AA; 35227 MW; 327B14A6EDDD2A02 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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                                                                                                                                 Query Match
Best Local Similarity 32.7%;
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CYSLT2.
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Matches
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                                                                                                                                   PSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
                                                                                                                                                                          HDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFITCYL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Furuichi K.; "The molecular characterization and tissue distribution of the human
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PEDELINE-20374466, PubMed-10913337;

Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota '
Nishikawa T., Kawai Y., Masuho Y., Isogai T., Suzuki Y., Sugano S.,
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 19, Last annotation update)
CYSTEINYL LEUKOTRIENE CYSLT2 RECEPTOR (BA108P5.1) (CYSTEINYL
BA108P5.1 OR CYSLT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nothacker H.-P., Wang Z., Zhu Y., Civelli O.;
"Identification, Molecular Cloning and Characterization of Human Cysteinyl Leukoriene Receptor.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB018269; BAB03601.1;
EMBL; AF254664; AAG17281.1;
EMBL; AF279611; AAK69485.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cysteinyl leukotriene CysLT2 receptor.";
Biochem. Biophys. Res. Commun. 274:316-322(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 AA
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InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                          295 CSLKPKQPGHSKTQ 308
                                                                                                                                                                                                                                                                                                                                              302 SALRKGHPOKAKTK 315
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120 PHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC---ESFIMESANGW 176
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                            27 NSRNCTIE-NPKREFFPIVYLIIFFWGVLGNGLSIYVF---LQPYKKSTSVNVFMLNLAI
                                                                                                ADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVH
  NGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLAV
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Sus.
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB652662; BAB60817.1; -
SEQUENCE 345 AA; 39410 MW; 5D1B1FB89B895905 CRC64;
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Cetartiodactyla; Suina; Suidae;
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Last annotation update)
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(TrEMBLrel. 19, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 CSLKPKQPGHSKTQ 308
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                     Receptor.
                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T., Ohishi T., Soga T., Matsushime H., Furuichi K.; "Characterization of the cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 HPHHAVNTISTRVAAGIVC-TLWALVILGTVYLLLENHLCVQETAVSCESFIMESAN--G 175
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                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Chondrichthyes;
Elasmobranchii: Squalea: Hypnosqualea: Pristiorajea; Batoidea;
Rajiformes: Rajidae: Raja.
NCBI_TaxID=7782;
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Dranoff J.A., O'Nelll A.F., Franco A.M., Cai S.Y., Connolly G.C.,
Ballatori N., Boyer J.L., Nathanson M.H.;
A printitive ATP receptor from the little skate Raja erinacea.";
J. Biol. Chem. 275:30701-30706(2000).
EMBL; AF242850; AAG42684.1;
HSSP; P34996; IDDD.
InterPro; IPR000276; GPCR_Rhodpsn.
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB052661; BAB60816.1; -. SEQUENCE 309 AA; 35507 MW; A122AC8177879D56 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                          309 AA
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                                                                                                                                                            Created)
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                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
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78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                  T-LWALVILGTVYLLL-----ENHLCVQETAVS-CESFIMESANGWHDIMFQLEFF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP----SVSA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTDWIFGDALCKLORFLFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKKNSIYISA 161
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                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                           212 IPFATILVCYGFIVKALISNDM--KTPLRGKSVRLVIIVLAVFAISYLPFHVMKNLNLQS
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                              29;
                                                                                                                                                     18.5%; Score 342.5; DB 13; Length 357; 26.4%; Pred. No. 4.5e-26; Live 69; Mismatches 144; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 361;
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                                                                                                          41239 MW; 14604EE15DCBDB41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOMN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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29.0%; Pred. No. 6.4e-26;
tive 61; Mismatches 135;
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                                                                                                                                                                                                            87; Conservative
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                                                                                                          357 AA;
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Matches 87; Conserv
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Best Local Similarity 31.8%;
Matches 95; Conservative
PRELIMINARY;
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                                                                                                                               NCBI_TaxID=9606;
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Than novel orphan G-protein coupled receptor primarily expressed in the brain is localized on human chromosomal band 2q21.";
Than is localized on human chromosomal band 2q21.";
J. Neurochem. 1998:1357-1365(1998).
BMBL; Y12546; CAA73144.1;
BMBL; Y12546; CAA73144.1;
R HSSP; P34996; lDDD.
R Interpro; IPR000276; GPCR_Rhodpsn.
PRIMTS; PR0017; Tru_1; 1.
R PROSTIE; PS0001; 7fu_1: 1.
R PROSTIE; PS00237; GPCRHODOPSN.
R PROSTIE; PS050237; GPROTEIA_RECEP_FI_2; 1.
R RCSTIE; PS050263; G_PROTEIA_RECEP_FI_2; 1.
R RCSTIE; PS050263; G_PROTEIA_RECEP_FI_2; 1.
R RCSTIE; PS050263; G_PROTEIA_RECEP_FI_2; 1.
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                                        217 PFILILGCYGLIVRALIYKDMNNAPLR-KKSIYLVIIVLTVFAVSYLPFHVMKNLNLRAR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
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                                                                                    LKLRRPLYAHLACAFLWVVAVANAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 AFTFPFITTVTCYLLIIRSL--RQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL
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                                                                   LYFLWTVPSSAC - - DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK
                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.1%; Score 336; DB 4; Length 367; 30.5%; Pred. No. 2.1e-25;
                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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            PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-
                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                 367
                                                                                                                                                                                                                                                                                                    P2Y-LIKE G-PROTEIN COUPLED RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                              330 ASRRSEANVQSKSEEVTLNIL 350
                                                                                                                            299 PKQPGHSKTQ-RPEEMPISNL 318
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                                                                                                                                                                                                                                 PRELIMINARY;
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Matches
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TISSUE-BRAIN;
MEDLINE-20453044; PubMed-10996426;
Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
"Molecular cloning and expression of a type-two somatostatin receptor in goldfish brain and pituitary.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Carassius.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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31.8%; Pred. No. 2.6e-25;
.ive 50; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 AA; 33397 MW; 36DAD60B157B9EDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
"A novel orphan G-protein coupled receptor primarily
aria is localized on human chromosomal band 2q21.";
J. Neurochem. 1998:1357-1365(1998).
EMBL; 294155; CABO8108.1; -.
01.MAY-2000 (TrEMBLrel. 13, Created)
01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.JUN-2001 (TrEMBLrel. 17, Last annotation update)
P2Y-LIKE G-PROTEIN COUPLED RECEPTOR (FRAGMENT).
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1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOCATAIN RECEPTOR TYPE TWO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODPSN.
PROSITE; PS00237; G_POTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
ROCEPTOR; G-Protein coupled receptor.
NON_TER
SEQUENCE 298 AA; 33397 MW; 36DAD60B157B9EDB CR
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Nature 409:685-690(2001)
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MEDLINE-2108560; PubMed-11217851;

MEDLINE-2108560; PubMed-11217851;

MEDLINE-2108560; PubMed-11217851;

MATARAW J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsudi F., Suzuki R., Tomita B., Kochiwa H.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J. Bult C., Fletcher C., Fullita M., Gariboldi M.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mayashizaki Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLIVICMCYLLIVIKVKSSGMRVCSSKRKRSERKVTRMVSIVVVVFVLCWLPFYVFNVTS 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 PLGIILFCSFKIVWSLR----RRQQLARQARMKKATRFIMVVAIVFITCYLP-----S 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                   1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROPEIN (BY SIMILARITY).
1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

EMBL, AF19397; AAF98367.1; -.

PINTERPO. IPRO00237; GPCR_Rhodpsn.

PRO171F; PR00237; GPCRRHODPSN.

PROSITE; PS00237; GPCRRHODPSN.

PROSITE; PS00267; G_PROTEIN_RECEP_F1_1; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.

SEQUENCE 380 AA: 43146 MW; CE897FF7537CFA30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 TISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 VSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKL 292
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                              ch 17.8%; Score 329.5; DB 13; Length 380; 1 Similarity 31.0%; Pred. No. 9.6e-25; 92; Conservative 52; Mismatches 126; Indels 27;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PURINERGIC RECEPTOR P2Y, G-PROTEIN COUPLED 2.
Endocrinol. 166:75-87(2000)
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Matches 9
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Q9CP24;
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82 YAASLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHS 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 IVFITCYLP-SVSARLYFLWTVPSSACDP--SVHGALHITLSFTYMNSMLDPLVYYFSSP 283
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                                                                                                                                                                                                                                                                                                                                                                                                             34;
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EMBL; AK015738; BA33719.1; -.
EMBL; AK055013; BAB23746.1; -.
HSSP; P34996; 1DDD.
MGD; MG1:105107; PZY2.
InterPro; IPR000276; GPCR_Rhodpsn.
PFGMI; PR000217; GPCR_Rhodpsn.
PRINTS; PR00237; GPROTEIN_RECEP_FI_1; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_2; 1.
SEQUENCE 373 AA; 42188 MW; E4BD653D895DCE8F CRC64;
                                                                                                                                                                                                                                                                                                                                             Query Match 17.1%; Score 317; DB 11; Best Local Similarity 29.8%; Pred. No. 1.7e-23; Matches 97; Conservative 45; Mismatches 150;
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Job time : 75 secs
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Human nGPCR11 cod

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RESULT 1
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cDNA encoding HM74
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SIDS1/gcgdata/geneseq/geneseqn-embl/Na1981.DaT:*
SIDS1/gcgdata/geneseq/geneseqn-embl/Na1981.DaT:*
SIDS1/gcgdata/geneseq/geneseqn-embl/Na1981.DaT:*
SIDS1/gcgdata/geneseq/geneseqn-embl/Na1984.DaT:*
SIDS1/gcgdata/geneseq/geneseqn-embl/Na1984.DaT:*
SIDS1/gcgdata/geneseq/geneseqn-embl/Na1981.DaT:*
SIDS1/gcgdata/geneseq/geneseqn-embl/Na1981.DaT:*
SIDS1/gcgdata/geneseq/geneseqn-embl/Na1981.DaT:*
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SIDS1/gcgdata/geneseq/geneseqn-embl/Na1981.DaT:*
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SIDS1/gcgdata/geneseq/geneseqn-embl/Na1991.DaT:*
SIDS1/gcgdata/geneseq/geneseqn-embl/Na1991.DaT:*
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                    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                   1736436 seqs, 858457221 residues
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Maximum Match 100%
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1041
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/product= "GPCR protein"
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06-SEP-2000; 2000US-230459P.
20-SEP-2000; 2000US-0666535.
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11-FEB-2000;
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                                                                                                Novel human G-protein coupled receptor proteins and nucleic acid molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the
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                  D1 Francesco V,
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Matches 1041; Conservative
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G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; achizophrenta; htyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neuronal disorder; neuronal disorder; attention deficit-hyperactivity disorder; Attention deficit disorder; parkinson's disease; mancer; parkinson's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence encodes a human G-protein coupled receptor (GPCR)
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14-MAR-2000; 2000US-0189258.
14-MAR-2000; 2000US-0189259.
10-APR-2000; 2000US-0195898.
10-APR-2000; 2000US-0195899.
10-APR-2000; 2000US-0196078.
12-MAY-2000; 2000US-0200419.
12-JUN-2000; 2000US-0210982.
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Matches 1041; Conservative (
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(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

28, 31-38, 40, 41, 53-60) and their coding sequences. The present

sequence is the coding sequence for one such G protein-coupled receptor.

GPCRs are also known as seven transmembrane receptors and function in

signal transduction. The nGPCRx coding sequences are useful for

screening a human to diagnose a disorder affecting the brain or a genetic

c predisposition, specifically schizophrenia. nGPCRx are useful for

identifying compounds useful for treating schizophrenia. Detection of

c for disposition, specifically schizophrenia. nGPCRx are useful for

c disporders in a sample is useful as a diagnostic tool for diseases or

c disporders, infections such as HIV-1, metabolic and cardiovascular

c diseases, proliferative disorders, renal failure, rheumatoria arthritis,

c nGPCRx activity have the utility for treating neurological disorders,

c including schizophrenia, ADHD/ADD (attention deficit-hyperactivity

disorder/attention deficit disorder), and neuronal disorders such as

c diseases, proliferative disorders, migraine and semile dementia.

Additional disorders include inflammatory conditions (e.g. Crohn's

c respiratory aliments auch as asthma, and inflammatory diseases e.g.
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Ez T, Huff
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V, Sejlitz T,
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                                                                                                                                                                                                                                                  Parodi LA,
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2000US-0188114.
2000US-0190310.
          99US-0166071.
99US-0166678.
99US-0173396.
2000US-0184129.
2000US-0185421.
2000US-0185554.
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2000US-0198568.
2000US-0201190.
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                                                22-FEB-2000;
28-FEB-2000;
28-FEB-2000;
02-MAR-2000;
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20-APR-2000;
02-MAY-2000;
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09-MAR-2000;
17-MAR-2000;
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28-DEC-1999;
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Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; annorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
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                                                                                                                                          TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
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                  GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
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                                                                       GGGAGCATCGTGCTTACGGTGGTGCCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
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Length 1050

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Sequence 1050 BP; 211 A; 299 C; 279 G; 261 T; 0 other;
                                                                                                                         Baumgartner JC, Gusev VY;
                                                                                                           CURA-) CURAGEN CORP.
                                                                                                                                 WPI; 2001-639351/73.
                                                                                                                                     P-PSDB; ABB44522
          WO200174904-A2.
                                           06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
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06-APR-2000; 2
                                                                  21-JUL-2000;
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28-JUL-2000;
   sapiens
                                        06-APR-2000;
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                                 31-MAR-2000;
                  11-0CT-2001
                                                                                                                   4ajumder K,
                                                                                                                      Padigaru M,
   Ношо
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The invention relates to nucleic acid sequences (ABAB1529-ABA81552) that encode G-coupled protein-receptor related polypeptides

(ABB44527-ABB44543). The isolated polypeptide having a sequence differing by no more than 15 % of amino acid residues from one of 22 amino acid capture forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences or sepecially defined in the collypeptides can be administered therapeutically, especially using gene polypeptides can be administered therapeutically, especially using gene captures, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atherosclerosis, disorders collosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's clasease, parkinson's disorder, Huntington's disease, multiple sclerosis, asthma, cancers, neurodegenerative disorders, immune disorders, hadmatopoietic disorders, developmental diseases, immune disorders, bacterial, fungal, protozoal and viral infections (e.g. with humans) by detecting alterations in polypeptide expression levels relative to control samples. They are useful to identify agents binding polypeptide control samples they are useful to identify agents binding polypeptide (e.g. callular receptors or deversament.)

control samples and agonists in disease areating activity, useful as modellating callular polypeptide expression or activity, useful as modellating callular polypeptide.
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11-OCT-2000; 2000US-236513P.
18-JAN-2001; 2001US-2652508P.
23-JAN-2001; 2001US-263433P.
23-JAN-2001; 2001US-263604P.
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can be administered therapeutically, especially using gene
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                                                                                                                                                                          anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabotes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
                                                                                                                                                                 GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;
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Li L;
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Spytek KA,
                                                                                                                                           Human GPCR1b polynucleotide SEQ ID NO 3.
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Padigaru M, Mishnu VS, Tchernev VT,
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            CACATTGTTGAGTGGCACTGA 1046
                                                                           ABA81530 standard; DNA; 1050 BP
1021 CACATTGTTGAGTGGCACTGA 1041
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06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
21-JUL-2000;
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28-JUL-2000;
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CECRX associated disorders, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atheosoclerosis, disorders related to signal processing and metabolic pathway modulation (e.g. obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disorders, developmental disease), immune disorders, neurodegenerative disorders (e.g. Alzheimer's bacterial, fungal, protozoal and viral infections (e.g. with human conferency virus (HIV)-1 or HIV-2). They can be used dispossitally to detecrine the presence of or predisposition to a disease associated with altered levels of the polypeptide expression levels relative to control samples. They are useful to redefice the public protozoal and disposition to a disease associated control samples. They are useful to redeficience of or predisposition to a disease associated (e.g. cellular receptors or downstream effectors) and/or agents modulating cellular polypeptide expression or activity, useful as
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                                                                                                                                                          966 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1025
                                                                                                                                                                                                                                                                                                                      arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy; Alzhahaer's disease; parkinson's disease; cardiovascular disorder; atherosclerosis; hypertension; myocardial infarction; peptic ulcer; gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder; acquired immune deficiency syndrome; inflammatory disorder; infection; Addison's disease; allergy; Grave's disease; metabolic disorder; AlbS; diabetes; obesity; osteoporosis; gene therapy; GCREC-3; ss.
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                                                                   841 TCAAGCCCCTCCTTTCCCAAATTCTACAACAGCTCAAAATCTGCAGTCTGAAACCCAAG
                                           CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
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Au-Young J;
                                 781 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
                                                                                                                                                                                                                                                                                                              Human; G-protein coupled receptor 3; cell proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human mature GCREC-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Thornton M, Lu Y, Tribouley Walia NK, Nguyen DB, Yue H, Reddy R, Kallick DA, Tang TY,
                                                                                                                                                                                                                                                                                             Human G-protein coupled receptor 3 (GCREC-3) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag- a
product- "Human GCREC-3 protein"
3.138
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                        AAD26371 standard; cDNA; 1083 BP
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                                                                                                                                                                           1021 CACATTGTTGAGTGGCACTGA 1041
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2000US-206222P.
2000US-207566P.
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Khan FA, Gandhi
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02-JUN-2000;
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Elliott VS,
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collypeptides and polynucleotides. GCREC polypeptides are useful in screening compounds that modulate their activity. They are useful in the diagnosis, prevention and treatment of disorders which include cell proliferative disorders such as arteriosclerosis, hepatitis, myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia, lymphoma; neurological disorders such as epilepsy, isohaemic locarebrowscular disease, Alzheimer's disease, Pick's disease, dementia, Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, annesia; cardiovascular disorders such as arteriovenous fistula, atherosclerosis, hypertension, vascular tumnors, myocardial infarction, hypertensive heart disease, infective endocarditis, cardiomyopathy, myocarditis; gastrointestinal disorders such as dysphagia peptic oesophagitis, emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea, constipation, acquired immune deficiency syndrome (AIDS), hepatic dermestitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, cupysemm, Grave's disease, gout, multiple sclerosis, rheumaeich cupysemm, Grave's disease, gout, multiple sclerosis, rheumaeich cupysemm, Grave's disease, gout, multiple sclerosis, rheumaeich cupysamic disorders such as diabetes, obesity and osteoporosis; and viral infections such as diabetes, obesity and osteoporosis; and curral infections such as diabetes, obesity and osteoporosis; and curral infections such as diabetes, obesity and osteoporosis; and curral infections such as diabetes, obesity and osteoporosis; and curral infections such as diabetes, obesity and osteoporosis; and curral infections such as diabetes, obesity and osteoporosis; and curral infections arenavirus, bunyavirus. Polynoicedice of the hovention are compounded to the propertice of the propertice of the disorders such a
                                                                                                                        Novel G-protein coupled receptors and polynucleotides useful for diagnosis, treatment and prevention of disorders of cell proliferation, neurological, cardiovascular, metabolic disorders and viral infections
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                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human G-protein coupled receptor (GCREC)
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                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 112; 115pp; English.
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Matches 1041; Conservative
WPI; 2002-089844/12.
P-PSDB; AAE16172.
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/note= "G-protein coupled receptor"

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Kiao Y;
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                                                                                                                                                                                                                                                                                                             961 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
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                                                     GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
                                                                                                                                                                                           CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
                                                                                                                                                                                                                                                                                                     CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC
                                            TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
                                                                                                 TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
                                                                                                                    TGGAGCCTGAGGCGGAGCAGCAGCTGGCCAGCCAGGCTCGGATGAAGAAGGCGACCCGG
                                                                                                                                                        TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
                                                                                                                                                                                                                               CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding HM74-like G-protein coupled receptor (GPCR).
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/product= "HM74-like_GPCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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The invention describes a novel isolated polynucleotide (I) encoding a human HM74-like G-protein coupled receptor (GPCR) polypeptide. Reagents that regulate HM74-like GPCR are useful for modulating the activity of their regulate HM74-like GPCR are useful for modulating the activity of the regulate HM74-like GPCR are useful form modulating the activity of the protein in a disease selected from bacterial, fungal, protozoan, and viral infection, pain, cancer, anorexia, bulimia, asthma, central nervous consistence, asthma, inflammation, allergy, benign prostatic hypertension, papertension, angina pectoris, myocardial infarction, urinary retention, osteoporosis, ulcer, asthma, inflammation, allergy, benign prostatic hypertrophy, culcer, asthma, inflammation, allergy, benign prostatic hypertrophy, culcer, syndrome. The composition is also useful for treating consistence of multiple sclerosis and disorders such as anxiety, schizophrenia, manic depression, delirium, dementia and severe mental retardation. (I) or the HM74-like GPCR polypeptide are also useful for treating the above consists of alseases, susceptibility to diseases and abnormalities related to the consense of multiples in the nucleic acid sequences which may act as agonists or antagonists at the receptor site and which can be regulated to provide therapeutic effects. The polypeptide is also useful as a balt convide therapeutic effects. The polypeptide is also useful as a balt convide therapeutic effects. The polypeptide is also useful as a balt convidence who have a provide therapeutic effects. The polypeptide is also useful as a balt convidence of muchapeutic effects. The polypeptide is also useful as a balt convidence of provide therapeutic effects. The polypeptide is also useful as a manmal convidence of muchapeutic effects. The polypeptide is also useful as a balt convidence of muchapeutic effects. The polypeptide is also useful as a manmal convidence of muchapeutic effects. The polypeptide is also useful as a manmal convidence of muchapeutic effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated polynucleotide, useful for treating infection, pain, cancer, asthma, hypertension, myocardial infarction, urinary retention, osteoporosis, encodes the human HM74-like G-protein coupled receptor polypeptide
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11arity 100.0%; Pred. No. 5.1e-288;
Conservative 0; Mismatches 0; Indels 0;
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WO200177320-A2.
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Matches 1041;
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hyperproliferative disorder; neurological disorder; psychiatric disease;
inflammatory disorder; respiratory disorder; gene therapy; ds.
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GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
       TGGAGCCTGAGGCGGAGGCAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
                         CACCACGCGGTGAACACTATCTCCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                         Gene encoding novel human G protein-coupled receptor (GPCR).
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The present invention relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor subfamily. The CDNA and gene sequences encoding for GPCR are also given in the invention. The sequences of the invention are useful for diagnosing and treating diseases or conditions mediated by human protected seases. Such diseases include hyperproliferative disorders.

(e.g. hyperplasia), neurological disorders (e.g. Parkinson's disease), psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g. diabetes) and respiratory disorders (e.g. alabetes) and respiratory disorders (e.g. alabetes) and respiratory disorders (e.g. diabetes) and respiratory disorders (e.g. alabetes) and respiratory disorders (e.g. diabetes) and respiratory disorders (e.g. alumen diag.) The GPCR protein is also useful for identifying a modulator of the expression of the protein. It also serves as a target for identifying agents for use in mammalian therapeutic applications, e.g. a mumund drug, particularly modulating a bological or pathological response in a cell or tissue that are related to members of the chemokine assays related to GPCRs that are related to members of the chemokine assays. GPCR is also useful in diagnosing a disease or predisposition to a disease mediated by the peptide, in pharmacogenomic analysis. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human G-protein coupled receptor proteins and nucleic acid molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents the human GPCR gene sequence of the invention.
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                                                                    2000US-192419P.
2000US-230459P.
2000US-0666535.
27-MAR-2001; 2001WO-US09522
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06-SEP-2000;
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                                                                                                                                         TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA 720
       GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
                        GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
                                                TCAAGCCCCTCCTTTCCCAAATTCTACAAGAGCTCAAAATCTGCAGTCTGAAACCCAAG
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                                                                                                         TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
                                                                                 Human GPCR1c polynucleotide SEQ ID NO 4.
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2000US-194614P.
2000US-195063P.
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05-APR-2000; 2
06-APR-2000; 2
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The invention relates to nucleic acid sequences (ABAB1529-ABAB1525) that encode G-coupled protein-receptor related polypeptides

CG (ABB44522-ABB44543). The isolated polypeptide having a sequence differing to more than 15% of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the completication and corresponding to human G-protein coupled receptor X (GPCRX) polypeptides. The polypeptides have potential cardiant, antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The colypeptides can be administered therapeutically, especially using gene therapy and expressing the encoding DNA in vivo, to treat or prevent CG GPCRX-associated disorders, especially in humans. For example, they can compare the colopies of the colopy and expressing and metabolic pathway modulation (e.g. cobesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple colopies, parkinson's disorder, Huntington's disease, parkinson's disorder, Huntington's disease, parkinson's disorder, Huntington's disease, immune disorders, contermine the presence of or predisposition to a disease associated content and evels of the polypeptide expression levels of the polypeptide expression levels callular receptors or flowestive to determine the bresence of or predisposition to a disease associated control samples. They are useful to identify agents binding polypeptide control samples or the polypeptide expression levels callular polypeptide expression levels finding polypeptide control samples. They are useful to identify agents binding polypeptide control samples or predisposition or activity, type, they are useful to describe a control samples. They are useful to a describe and a control samples or the polypeptide controls and the presence of the polypeptide controls and the presence of the polypeptide controls and the polypeptide appression levels and a dispersed and a control as the polypeptide controls and the pol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardlomyopathy or atherosclerosis, and to screen for antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Spytek KA,
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0; Mismatches 2;
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Mishnu VS, Tchernev VT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 11; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agonists useful therapeutically
06-APR-2000; 2000US-195066P.
06-APR-2000; 2000US-195067P.
06-APR-2000; 2000US-195068P.
06-APR-2000; 2000US-195070P.
06-APR-2000; 2000US-19510P.
21-JUL-2000; 2000US-21984P.
28-JUL-2000; 2000US-224588P.
11-AGG-2000; 2000US-224588P.
11-AGG-2000; 2000US-224588P.
11-AGG-2000; 2000US-224588P.
11-AGG-2000; 2000US-224588P.
11-AGG-2000; 2000US-224588P.
11-AGG-2000; 2000US-265508P.
23-JAN-2001; 2001US-265508P.
23-JAN-2001; 2001US-265644P.
29-MAR-2001; 2001US-263644P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639351/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Majumder K,
Padigaru M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The present invertion retarges to nover to protein coupleto inceptions to fore present invertion retarges to nover to protein coupleto inceptions as 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is the coding sequence for one such 6 protein-coupled receptor. Gedens are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for signal transduction. The nGPCRx coding sequences are useful for sometime a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. Detection of dentifying compounds useful for treating schizophrenia. Detection of copposition, specifically schizophrenia not agreed a disorders of insorders, infections such as HIV-1, metabolic and cardiovascular disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of copposition schizophrenia, ADHD/ADD (attention deficit disorder), and neuronal disorders such as include inflammatory conditions (e.g. Crohn's disease), rheumatolid arthritis, autolmmune disorders, cancers, concers, conce
                                                         G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; acchizophrenia; thyroid disorder; renal failure; rheumatoid arthitis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hiebsch RR, Lind P, Slightom J;
an CM, Ruff V, Sejlitz T, Huff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to novel G protein-coupled receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bannigan CM,
                 coding sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 77; 261pp; English.
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PS, Bannie
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2000US-0185554.
2000US-0186530.
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2000US-0188114.
2000US-0190310.
2000US-0190800.
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2000US-0201190
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                 nGPCR11
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19-NOV-1999;
28-DEC-1999;
22-FEB-2000;
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17-MAR-2000;
21-MAR-2000;
20-APR-2000;
02-MAY-2000;
08-MAY-2000;
25-MAY-2000;
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28-FEB-2000;
02-MAR-2000;
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The present sequence encodes a member of the G-protein coupled receptor. (TTM receptor) family, designated the HM/4A receptor. The proteins, agonists, antagonists and polynucleotides can be used for treating disorders associated with increased or reduced expression or activity of HM/4A, e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, cliabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia manic depression, depression, deliritum, dementia, and severe mental retardation, and dyskinesias such as Huntington's disease or cetardation, and dyskinesias such as Huntington's disease or cetardation, and control of the products can also be used for
                                                                HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension; asthma; allergy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 ATAGACAAGAAGTGCTGTGTTCCGAGATGACTTCATTGTCAAGGTGTTGCCGCCG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated G-protein coupled receptor, HM74A - used to develop products for treating e.g. infections, pain, cancers, diabetes, obesity, neurological disorders, heart failure, hypertension, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
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0; Mismatches 316; Indels
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                                  coupled receptor HM74A encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                      DJ, Elshourbagy NA, Guerrera SF,
                                                                                                                                                                                                                    "HM74A receptor"
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                                                                                                                                                                  Location/Qualifiers
61..1152
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                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                     97US-0049480.
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nes 600; Conservative
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(first entry)
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 29-APR-1999
                                                                                                                                      Homo sapiens
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                                    G-protein
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                                 Length 888;
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Sequence 888 BP; 174 A; 254 C; 231 G; 229 T; 0 other;
                               85.3%; Score 888; DB 22; L
100.0%; Pred. No. 2.7e-244;
ive 0; Mismatches 0;
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                                                                  Conservative
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                                                                                                                  517 GCCATCACTATTGGCCTGACAGTCCACCTCCTGAAGAAGAAGATGCCGATCCAGAATGGC
                                                                                                                                                                                                                                                                                                       541 TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
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                                                                                                                                                                    CACCACGCGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
                                                                                                 GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 766 GTCCATGGGGCCCTGCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; G-protein coupled receptor; GPCR; hRUP25; agonist;
inverse agonist; lung cancer; ss.
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The sequence encodes a human G-protein coupled receptor (GPCR), hRUP25. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
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Pred. No. 1.6e-95;
0; Mismatches 318; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1092 BP; 223 A; 320 C; 273 G; 276 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 71; Page 120-121; 159pp; English.
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2000US-0181749
2000US-0189259
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99US-0166369.
99US-0171900.
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P-PSDB; AAU04379.
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Best Local Similarity
Matches 598; Conserv
                                                                                                                                         23-DEC-1999;
23-DEC-1999;
11-FEB-2000;
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14-MAR-2000;
10-APR-2000;
10-APR-2000;
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20-OCT-2000;
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12-MAY-2000;
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26-SEP-2000;
16-NOV-2000;
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                                             TGGAGCCTGAGGCGGAGCCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
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                                                                                                                            GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
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                                 GGGAGCATCGTGCTTACGGTGGTGGCTGCCGACAGGTATTTCAAAGTGGTCCACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               886 AGTCTGAAACCCAAGCAGCCAGGACACTCAAAAA 919
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90677 and AAY90677 and AAA30709-A30743 and AAA30779-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous anno acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence or Ala, and is preferably Lys. When the endogenous residue at this Argor Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Argor preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Promay be endogenous. An endogenous, or a mixture of endogenous and con-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful for identifying antagonists. The mutant proteins are also useful for settings for elucidating the roles of the receptors in normal and discassed and discates associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous in an exemplification of the invention. This was cloned and subjected unstant of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                               Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 4.7e-95;
0; Mismatches 319; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1164 BP; 246 A; 337 C; 288 G; 293 T; 0 other;
                                                                                                                                                                                              Example 1; Page 185; 341pp; English.
                  Liaw CW;
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Best Local Similarity 63.9%;
Matches 597; Conservative (
                DT,
                Chalmers
                                                       WPI; 2000-329165/28
                                                                            P-PSDB; AAY90637
                  Behan DP,
                                                                                                                                                           agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                           DNA encoding human mutant G protein-coupled receptor HM74 (1230K).
                                    517 CCTGCAAATGTGTGCATCAGCTTCAGCATCTGCCATACCTTCCGGTGGCACGAAGCTATG
                                                   TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
                                                                                  TGGAGCCTGAGGCGGAGGCAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
                                                                                          TTCATCATGGTGGTGGCAATTGTGTTCATCATGCTACCTGCCCAGCGTGTCTGCTAGA
                                                                                                                       CTCTATITCCTCTGGACGGTGCCCTC------GAGTGCCTGCGATCCCTCT
                                                                                                                                                            754 ATCCGCATCTTCTGGCTCCTGCACATTCGGGCACGCAGAATTGTGAAGTGTACCGCTCG
                                                                                                                                                                           814 GIGGACCIGGCGTICTITATCACTCTCAGCTTCACCTACATGAACAGCATGCTGGACCCC
                                                                                                                                                                                                         826 CTGGTGTATTATTTTCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGC
                     G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist; mutant; ss.
                                                                                                                                                                                                                                        886 AGTCTGAAACCCAAGCAGCCAGGACACTCAAAAA 919
                                                                                                                                                                                                                                                       934 TGCCTCCAGAGGAAGATGACAGGTGAGCCAGATA 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 285-286; 341pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liaw CW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-329165/28.
P-PSDB; AAY90672.
                                                                                                                                                                                                                                                                                                                                                                                                              WO200022129-A1.
                                                                                                                                                                                                                                                                                                                           21-AUG-2000
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The invention relates to constitutively acree throughous versions of endogenous human orphan G protein coupled receptors (GPCRs, AAY90643-A3079). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous residue in IC3 at a position in amino acid X-(AA)15-pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Promogonius residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research setting for succeptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively acidive, they can be used directly for screening of compounds without the need for endogenous ingaids. Sequences AAA30793 and AAA30779 represent DNAs
invention relates to constitutively active, non-endogenous versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCAGCATCATCTTCCTCACGGTGGTGGCGGTAGACAGGTATTTCCGGGTGGTCCATCCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        577 Trecreeredagricerecreeceredecarearergricarecreererageaarrare 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCTCATTGTGGCCTTTGTGCTGGCGCCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1164 BP; 248 A; 335 C; 289 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 366; DB 21; 1
Pred. No. 1.3e-94;
0; Mismatches 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding the mutant human GPCRs of the invention.
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63.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.89
Matches 596; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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TGGAGCCTGAGGCGGAGGCAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGAGCCGGG

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us-09-886-041-1.std.rng

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Consensus sequences are identified from nine rat gene receptors. The receptors are for somatostatin, substance K, substance P, neuromedin K, thyrotropin, HH/CG and others designated mas, mrg and rta. Four regions of nucleotide sequence are found to exhibit a degree of conservation significant enough to design degenerate oligo primers for PCR (see AAQ55045-49). Five oligos are designed with 4 - to 64-fold direct degeneracy plus 5%-23% inosines. The oligos are designed to anneal sequences in G protein-linked peptide receptor genes. They are used as six different primer pairs for PCR using rat genomic DNA
                                                                                                               754 Arccecarcricrescrecrecacartressecacecagaartstsaagretacescres 813
                                                                                                                                                                                                                     874 GIGGIGIACTACTICTCCAGCCCATCCTTTCCCAACTTCTTCTCCACTTTGATCAACCGC 933
TGGAGCCTGCGGCAGAG---ACAAATGGACCGGCATGCCAAGATCAAGAGCCAAAACC 693
                         GTGGACCTGGCGTTCTTTATCACTCTCAGCTTCACCTACATGAACAGCATGCTGGACCCC
                                                                                                                                                                                                    CTGGTGTATTATTTTCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGC
                                                                                    CTCTATTTCCTCTGGACGGTGCCCTC------GAGTGCCTGCGATCCCTCT
                                                                                                                                             GTCCATGGGGCCCTGCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolation and identifying new receptor DNA - pref. G-protein linked receptors, using PCR with new receptor specific primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer; peptide ligand receptor; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                   orphan receptor DNA fragment PCR
                                                                                                                                                                                                                                                            886 AGTCTGAAACCCAAGCAGCACGACACTCAAAAA 919
                                                                                                                                                                                                                                                                              /*tag= b
/label= PCR oligo no. 10
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1..26
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/label= PCR oligo no. 526..545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMCY ) AMERICAN CYANAMID CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ozenberger BA,
                                                                                                                                                                                                                                                                                                                                                               AAQ55054 standard; DNA; 546
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                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR; oligo;
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as template. All six reactions produce DNA fragments of the expected size. DNA fragments are cloned and two samples, designated PCR9 and PCR11(AAQ55054,Q55065), are found to contain sequences characteristic of g protein-linked receptors. Each fragment contains a single ORF. There is considerable similarity between rat somatostatin receptor and PCR11, suggesting that PCR11 is a novel somatostatin receptor subtype. Both fragments exhibit not only primary sequence similarity to other receptors but also the hydropathy pattern characteristic of G protein-linked receptors. The novel G protein-linked receptors are possibly of the peptide ligand subclass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGACAACTATGTCCAGAACTGGGACTGGGGAGCATCCCCTGCCGCGGGATGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTGGCATCGTCTGCACCCTGTGGGCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 CACGGACATGATGACCCGAAACGGCGATGCAAACCTGTGCAGCAGTTTTAGCATCTGCTA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTCGGATGAAGAAGGCGACCCGGTTCATCATGGTGGTGGCAATTGTGTTCATCACATG 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTCAAGATCAAGAGGGCCATCAACTTCATCATGATGGTGGTTGTCATTGTGTTTGCCATCTG 537
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                  1 TTCGTGGTGAACCTGGTCGGGGCTGACTTTTCTCCTGATCATTTGCTTTGCCTTCTTGAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 CAGGTATTTCAAAGTGGTCCACCCCCACGCGGTGAACACTATCTCCACCGGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                         216 AGACTATTACCTCAGACGTAGACACTGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCACGTTGGCCATGAACAGGGCCGGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 GGAGAACCATCTCTGCGTGCAAGAGACGGCCGTCTCCTGTGAGAGCTTCATCATGGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTATTTTGCTCCTTCAAGATTGTTTGGAGCCTGAGGCGGAGGCAGCAGCTGGCCAGACA
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                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                               DB 15; Length 546;
                                                                                                                                                                                                                                                             Score 220.2; DB 15; Length
Pred. No. 5.9e-53;
0; Mismatches 188; Indels
                                                                                                                                                                                                                          Sequence 546 BP; 106 A; 157 C; 144 G; 139 T; 0 other;
                                                                                                                                                                                                                                                             Query Match 21.2%;
Best Local Similarity 65.0%;
Matches 357; Conservative
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CTGGCTGCC 546
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October 29, 2002, 03:44:28; Search time 61 Seconds (without alignments) 630.025 Million cell updates/sec
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1853
1 MINGSCCRIEGDTISQVMPP......ANSFQSQSDGQWDPHIVEWH 346
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1. (SIDSI) gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
2. (SIDSI) gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
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20. (SIDSI) gcgdata/geneseqy-embl/AA1999.DAT:\*
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24. (SIDSI) gcgdata/geneseqy-embl/AA1999.DAT:\*
25. (SIDSI) gcgdata/geneseqy-embl/AA1999.DAT:\*
27. (SIDSI) gcgdata/geneseqy-embl/AA1999.DAT:\*
27. (SIDSI) gcgdata/geneseqy-embl/AA1999.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human GPCR1a polyp	Novel human G prot	Human G-protein co	Human nGPCR11 #2.	Human GPCR1c polyp	Human nGPCR11 #1.	G-protein coupled	Human G-protein co	Human mutant G pro	Human G protein-co	Human CON103 G pro
SUMMARIES	ΙΩ	ABB44522	AAU06197	AAU04373	AAG80968	ABB44523	AAG80934	AAW94654	AAU04379	AAY90672	AAY90637	AAE02493
		22	22	22	22	22	22	20	22	21	21	22
	Query Match Length DB	346	346	346	346	346	296	363	363	387	387	384
æ	Query Match	100.0	100.0	100.0	100.0	99.5	84.7	47.7	47.7	47.6	47.5	28.5
	Score	1853	1853	1853	1853	1839	1570	883.5	883.5	881.5	880.5	529
	Result No.	-1	~	m	₹	S	ø	7	æ	6	10	11

Human 7-transmembr		Human G-protein co	Human cell surface	Human 7-transmembr		Human G protein-co	Human mutant G pro	Human G-protein co	Human G-protein co	Human G-protein co	Human P2Y-like GPC	Human G-protein co	Human G-protein co	Human G-protein co	Cysteinyl leukotri	Human LTC4 recepto	Pig LTC4 receptor	Human G-protein co	Truncated cysLT2 c	Human cysLT2 cyste	Rat cysLT-like rec	Rat LTC4 receptor	2	Human 7-transmembr	Seven transmembran	Human G-protein th	Human R12 seven tr	Human 7TM receptor	Human G protein-co	Human P2Y-11ke GPC	Human mutant G pro	Human G protein co	Himan reporter-age
AAW88460	78	9	c	AAW88461	S	AAY90625	AAY90659	9	AAE07539	AAE12022	AAB82852	AAE07538	AAU04368	AAU04383	AAU07294	AAB73097	AAB73098	AAE08553	AAB85097	AAB85094	AAB85095	AAB73099	AAE04389	AAW62597	AAR53752	AAW07617	AAW48733	AAB21697	AAY90618	AAB82853	AAY90652	AAY79576	AAY69989
20	22	22	21	20	21	21	21	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	19	15	18	19	21	21	22	21	21	21
423	423	423	455	476	319	319	319	319	341	346	346	346	346	346	346	346	345	346	331	347	309	309	373	370	339	339	339	339	339	339	339	309	309
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529	529	529	529	510	451.5	448.5	448.5	448.5	366.5	366.5	366.5	366.5	366.5	366.5	366.5	366.5	362	361.5	357	357	355.5	355.5	354	346.5	336	336	336	336	336	336	335	327	327
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	58	53	30	31	35	33	34	32	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

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anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; ancrexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzhelmer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV.
                                                                                                            G-coupled protein-receptor; cardiant; antiarteriosclerotic;
                                                                                       Human GPCRla polypeptide SEQ ID NO 2.
                       Ź
                     ABB44522 standard; Protein; 346
                                                                                                                                                                                                                                                                                 2000US-194614P.
2000US-195063P.
2000US-195066P.
2000US-195067P.
                                                                                                                                                                                                                                                                                                                             2000US-195068P.
2000US-195069P.
2000US-195070P.
                                                                                                                                                                                                                                                                                                                                                              2000US-195510P.
2000US-219855P.
                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US10241
                                                                 (first entry)
                                                                                                                                                                                                      WO200174904-A2.
                                                                                                                                                                                                                                                                                 05-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
                                                                                                               Human; GCPR;
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              06-APR-2000;
21-JUL-2000;
                                                                                                                                                                                                                                                                       31-MAR-2000;
                                                                 28-JAN-2002
                                                                                                                                                                                                                            11-OCT-2001
                                           ABB44522;
RESULT 1
ABB44522
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181 FQLEFFMPLGIILF@SFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

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rotein; 346

AAU06197 standard;

RESULT 2 AAU06197

SNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346

OPGHSKTORPEEMPA

301

S G S

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The invention relates to nucleic acid sequences (ABAB1529-ABAB1552) that encode Groupled protein-receptor related polypeptides acquence differing (ABB44522-ABB4443). The isolated polypeptide having a sequence differing by no more than 15 % of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the completion of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the completion of the sequences (or present or present of the sequences) and instruction of the sequence of the sequences or present or present cardiomyopathy, atherosclerosis, disorders related to signal processing and metabolic pathway modulation (e.g. cobesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple cobesity, anorexia, dishaman, diabetes, osteoporosis, Crohn's disease, multiple cobesity, anorexia, dishaman, diabetes, osteoporosis, crohn's disease, multiple cobesity, anorexia, the sequence of or predisposition to a disease associated to determine the presence of or predisposition to a disease associated control samples. They are useful to identify agents binding polypeptide control samples. They are useful to identify agents binding polypeptide control samples. They are useful to identify agents binding polypeptide control samples or benefactors and control samples. They are useful to destrain a ceceptors or downstream effectors and control are to be the profession levels of cellular receptors or downstream effectors and control are to be the profession and a disease associated control samples. They are useful to identify agents binding polypeptide control samples are a protein and a disease associated control samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modulating cellular polypeptide expression or activity, useful as antagonists and agonists in disease treatment
                                                                                                                                                                                                                                                                          Spaderna SK;
Li L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1853; DB 22; Length 346; 100.0%; Pred. No. 1.2e-199;
                                                                                                                                                                                                                                                                          Wolenc AR,
Spytek KA,
                                                                                                                                                                                                                                                                          Casman SJ,
Tchernev VT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agonists useful therapeutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 8; 157pp; English.
                   2000US-221325P.
2000US-224588P.
2000US-239613P.
2001US-265508P.
2001US-263433P.
                                                                                                                                                        2001US-265161P
                                                                                                                                                                             29-MAR-2001; 2001US-0823172
                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639351/73.
N-PSDB; ABA81529, ABA81530.
                                                                                                                                                                                                                                                                                                                     Baumgartner JC, Gusev VY;
                                                                                                                                                                                                                                                                          Vernet CAM,
                                                                                                                                                                                                                                                                                                  Mishnu VS,
                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 AA;
                                                                                                           23-JAN-2001;
23-JAN-2001;
                                          11-AUG-2000;
11-OCT-2000;
                                                                                        18-JAN-2001;
                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                        Majumder K,
Padigaru M,
                                                                                                                                                                                                                                                                                                  Padigaru
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Human, G-protein coupled receptor; GPCR; chemokine receptor; protease; hyperproliferative disorder; neurological disorder; psychiatric disease; inflammatory disorder; respiratory disorder.

in-coupled receptor (GPCR) protein.

Novel human G prote

entry)

(first

19-DEC-2001

AAU06197;

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Ner; 2001-616503/71.

N-PSDB; AAS12581.

Novel human G-protein coupled receptor proteins and nucleic acid addignostic compositions and for identifying modulators of the and diagnostic compositions and for identifying modulators of the and diagnostic compositions and for identifying modulators of the rotein and diagnostic compositions and for identifying modulators of the protein relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor coupled receptor (GPCR) which is related to the invention are useful coupled receptor (GPCR) which is related to the invention are useful coupled receptor (GPCR) which is reading diseases or conditions mediated by human proteases. Such diseases include hyperproliferative discretars (e.g. hyperplasia) neurological disorders (e.g. Parkinson's disease), softworhistric diseases (e.g. Schizophrenia), inflammanchy disorders (e.g. diabetes) and respiratory disorders and respiratory distract to fittle expense in a related to members of the chemokine receptor subfamily, in drug screening assays and in competition to disease mediated by the peptide, in pharmacogenomic analysis. The polynucleotide sequences
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Gaps

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Indels

Mismatches

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Matches 346; Conservative

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61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

121 121 181

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FQLEFFWPLGIILFCSFKIVWSLRRRQQLARQARWKKATRFIMVVAIVFITCYLPSVSAR 240

346 AA

Sequence

Beasley EM;

Di Francesco V,

Ye J, Cravchik A,

(PEKE ) PE CORP

27-MAR-2000; 2000U\$\frac{3}{2}-192419P. 06-SEP-2000; 2000U\$-230459P. 20-SEP-2000; 2000U\$-0666535.

27-MAR-2001; 2001W@-US09522

Homo sapiens. WO200173029-A2.

04-OCT-2001.

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The sequence represents a human G-protein coupled receptor (GPCR), hRUP19. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                               receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signal transduction; schizophrenia; thyroid disorder; renal failure, rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; harmonal disorder; attention deficit-hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFLLMICLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARWKKATRFIMVVAIVFITCYLPSVSAR
                                                                                                  Endogenous and non-endogenous versions of human G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor; nGPCR; seven transmembrane receptor;
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1853; DB 22; Length 346; 100.0%; Pred. No. 1.2e-199; Ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGWDPHIVEWH 346
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                                                                                                                                                           Claim 45; Page 110-111; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG80968 standard; Protein; 346
                            Lowitz KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 346; Conservative
(AREN-) ARENA PHARM INC.
                                                       WPI; 2001-355616/37
                            Dang HT,
                                                                                                                                                                                                                                                                                                                                                   346 AA;
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                                                                     N-PSDB; AAS07946
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                            Chen R,
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                                                                                                                                                                                                                                                                                                                      Gaps
                                                                     MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
                                                                                  1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
                                                                                                                                                                                                                                            FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
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             Length 346;
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                                          Indels
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                                                                                                                                                                                                                                                                                                                                                               QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
          100.0%; Score 1853; DB 22;
100.0%; Pred. No. 1.2e-199;
:Ive 0; Mismatches 0;
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2000us-0210982.
2000us-0226760.
2000us-0235418.
2000us-0245779.
2000us-0242332.
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99US-0166369.
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2000US-0181749.
2000US-0181749.
2000US-0189258.
2000US-0189259.
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2000US-0196078.
2000US-0200419.
2000US-0203630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inverse agonist; lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                        al Similarity 100.
346; Conservative
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26-SEP-2000;
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28-APR-2000;
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23-DEC-1999;
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            Query Match
Best Local S
Matches 346
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Gaps

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Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disease; Huntington's disease;
61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                                                 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM
                                                                                                                                                                          LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK
                                                                                                      FOLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
                                                                                                                                                                                                                                                                   301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infection; human immunodeficiency virus; HIV.
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Mishnu VS, Tchernev VT,
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                                                                                                                                                                                                                                                                                                                                                                        ABB44523 standard; Protein; 346
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2000US-195063P.
2000US-195066P.
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2000US-195068P.
2000US-195069P.
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2000US-195510P
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2000US-221284P
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2000US-224588P
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2001US-263433P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639351/73.
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06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
21-JUL-2000; 2
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06-APR-2000;
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28-JUL-2000;
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Padigaru M,
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(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

28, 31-38, 40, 41, 53-60) and their coding sequences. The present

sequence is one such G protein-coupled receptor: GPCRs are also known as

c seven transmembrane receptors and function in signal transduction. The

c nGPCRx coding sequences are useful for screening a human to diagnose a

disorder affecting the brain or a genetic predisposition, specifically

c chizophrenia. nGPCRx are useful for identifying compounds useful for

treating schizophrenia. Detection of nGPCRx in a sample is useful as a

diagnostic tool for diseases or disorders e.g. thyroid disorders, renal

failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,

metabolic and cardiovascular diseases, proliferative disorders and

c treating neurological disorders, including schizophrenia, ADHD/ADD

c treating neurological disorders, including schizophrenia, ADHD/ADD

c (attention deficit hyperactivity disorder/attention deficit disorder),

and neuronal disorders such as Alzheimer's disease, Parkinson's disease,

migraine and senile dementia. Additional disorders include inflammatory

c conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune

diseases e.g. inflammatory bowel disease.
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Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
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2000US-0190800.
2000US-0198568.
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2000US-0186811.
2000US-0188114.
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99US-0166071.
99US-0166678.
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PS, Ba
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2000US-0185421.
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neuroprotective.
                                                                  WO200136473-A2.
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Schellin KA,
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03-MAR-2000;
09-MAR-2000;
                                  Homo sapiens.
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21-MAR-2000;
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28-FEB-2000;
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08-MAY-2000;
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New human G-protein coupled receptor X, GPCRX, polypeptide useful in

N-PSDB; ABA81531

DFLLMICLPFRTDYYLKRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

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Spaderna SK; Li L;

Wolenc AR, Spytek KA,

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The invention relates to nucleic acid sequences (ABA81529-ABA81552) that encode G-coupled protein-receptor related polypeptides as equence differing to more than 15 % of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the completication and corresponding to human G-protein coupled receptor X (GFCRX) polypeptides. The polypeptides have potential cardiant, antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The colypeptides can be administered therapeutically, especially using gene therapy and expressing the encoding DNA in humans. For example, they can be used to treat/prevent cardiomyopathy, atherosclerosis, disorders related to signal processing and metabolic pathway modulation (e.g. obesity, anorexia), diabetes, osteoporosis, crohn's disease, multiple colesity, anorexia, disorder, Huntington's disease, immune disorders, haematopoietic disorders, developmental diseases, neurological disorders, haematopoietic disorders, developmental diseases, neurological disorders, condetermine the presence of or predisposition to a disease associated control samples, they are useful to identify agents binding polypeptide control samples. They are useful to identify agents binding polypeptide control samples are perfectors or advisor or predisposition.
revention of GPCRX associated disorders e.g. or atherosclerosis, and to screen for antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (e.g. cellular receptors or downstream effectors) and/or agents modulating cellular polypeptide expression or activity, useful as antagonists and agonists in disease treatment.
  treatment or prevention of GPCRX
                                                                                                              Claim 1; Page 11; 157pp; English
                                                          agonists useful therapeutically
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61 DFLLMICLPFRTDXYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAAGRYFKVVHP 120 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120 Gaps 1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60 ; 0 99.2%; Score 1839; DB 22; Length 346; 99.4%; Pred. No. 4.7e-198; Indels 0; Mismatches Best Local Similarity 99.4 Matches 344; Conservative Query Match 61 121 g ò a ò g ò g ò à

301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGWDPHIVEWH 346 AAG80934 standard; Protein; 296 AA. (first entry) 28-AUG-2001 AAG80934; AAG8093/ RESULT DX DX SX

Human nGPCR11 #1

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301 OPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346

signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neurological disorder; neurological disorder; neuronal disorder; Alzhelmer's disease; cancer; attention defilott-hyperactivity disorder/attention defilott disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autolmmune disorder; respiratory allment; protein-coupled receptor; nGPCR; seven transmembrane receptor; neuroprotective

Homo sapiens.

WO200136473-A2.

25-MAY-2001

2000WO-US31581 16-NOV-2000;

17-NOV-1999; 19-NOV-1999;

2000US-0185554. 2000US-0186530. 2000US-0186811. 99US-0166071. 99US-0166678. 99US-0173396. 2000US-0201190. 2000US-0203111. 2000US-0190800 2000US-0198568 2000US-0190310 2000US-0185421 2000US-0188114 28-FEB-2000; 02-MAR-2000; 03-MAR-2000; 09-MAR-2000; 17-MAR-2000; 21-MAR-2000; 20-APR-2000; 08-MAY-2000; 22-FEB-2000; 28-FEB-2000; 02-MAY-2000; 28-DEC-1999; 

(PHAA ) PHARMACIA & UPJOHN CO

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346 AA;

Sequence

2000US-0207094

25-MAY-2000;

Hiebsch RR, Lind P, Slightom J; Bannigan CM, Parodi LA, PS, Banni Schellin KA, Kaytes ĽS, Wood Vogeli

WPI; 2001-389826/41. N-PSDB; AAH50974 New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia

Claim 37; Pages 77-78; 261pp; English.

treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease. The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their codding sequences. The present sequence is one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as a diagnositic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for

296 AA; Sequence

Query Match

Length 296; 84.7%; Score 1570; DB 22; severe mental

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12-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HM74A receptor; G-protein coupled receptor; infection; pain; cancer;
diabetes; obesity; neurological disorder; heart failure; hypertension;
                                                                                                            WAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLW 140
                                                                                                                             260
                          Gaps
                                                     LLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRH 80
                                                                                9
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                                                                    WSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSACDPSVHGAL
                                                                                                                                                                                                                                           present sequence is a member of the G-protein coupled receptor
                                                                                                                                                                       ALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLEFFMPLGIILFCSFKIV
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                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ×
           6.8e-168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SF,
          Pred. No. 6.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein coupled receptor HM74A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bergsma DJ, Elshourbagy NA, Guerrera
                                                                                                                                                                                                                                                                                                                                                                                         ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 31-32; 40pp; English.
100.08; Pre-
                                                                                                                                                                                                                                                                                                                                                                                      AAW94654 standard; Protein; 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US12386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0049480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-095273/08.
           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX16671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9856820-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                    AAW94654;
             Local
           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                241
                                                                                                            81
                                                                                                                                                                                                121
                                                     21
                                                                                                                                                                       141
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245 WIVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
                                                                                                                                                                                                                                                                                                                                                                             77 IICLPELMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136
                                                                                                                                                                                                                                                                                                                                                                                                                         NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
                                                                                                                                                                                                                                                                                                                                  65 MICLPFRIDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                   64
                                               for
                                                                                                                                                                                                                                            5 SCCRIEGDIISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL
manic depression, depression, delirium, dementia, and severe me retardation, and dyskinesias such as Huntington's disease or Gilles de la Tourett's syndrome. The products can also be used detection, diagnosis and drug screening.
                                                                                                                                                                                                   7;
                                                                                                                                                        Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; G-protein coupled receptor; GPCR; hRUP25; agonist;
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
                                                                                                                                                        20;
                                                                                                                                                     47.7%; Score 883.5; DB 20;
52.8%; Pred. No. 1.5e-90;
tive 47; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G-protein coupled receptor, hRUP25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU04379 standard; Protein; 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0203630.
2000US-0210741.
2000US-0210982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           990S-0166088.
990S-0166099.
990S-0166369.
990S-0171900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inverse agonist; lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-FEB-2000; 2000US-0181749.
14-MAR-2000; 2000US-0189258.
14-MAR-2000; 2000US-0189259.
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10-APR-2000; 2000US-0195899.
10-APR-2000; 2000US-0196078.
28-APR-2000; 2000US-0200419.
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                                                                                                                                                                                                   Conservative
                                                                                                                                                                        Local Similarity
nes 180; Conserva
                                                                                                             363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200136471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999;
23-DEC-1999;
23-DEC-1999;
23-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-2000;
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245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
agonist; antagonist; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                   The sequence represents a human G-protein coupled receptor (GPCR), hRUP25. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settlings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                                                                                                                       Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 MICLPFRIDYYLRRHWAFGDIPCRVGLFILAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCCRIEGDTISOVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 WIVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.7%; Score 883.5; DB 22; Length 52.8%; Pred. No. 1.5e-90; ive 47; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human mutant G protein-coupled receptor HM74 (1230K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
                                                                                                                                                                                                                                                                        Claim 69; Page 121-122; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY90672 standard; Protein; 387 AA.
           2000US-0235418.
2000US-0235779.
2000US-0242332.
2000US-0242343.
                                                                                                                           Lowitz KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 52.8
Matches 180; Conservative
                                                                                           (AREN-) ARENA PHARM INC
                                                                                                                                                        WPI; 2001-355616/37
                                                                                                                          Dang HT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 AA;
                                                                                                                                                                           N-PSDB; AAS07952.
                            26-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2000
             26-SEP-2000;
                                                             20-OCT-2000;
                                            20-OCT-2000;
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                                                                                                                          Chen R,
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AAY90672
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cc and AAN90573-30709). The mutant protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAN90683-Y90687), and to DNA encoding them (AAA30709-A30743-AAY90677). The mutant protein comprising them (AAA30709-A30743-A30709). The mutant protein comprising intracellular loop 3 mutation in a portion of the protein comprising intracellular loop 3 cc 153 and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino cc acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, H1s, Arg or AA)15-Pro. The endogenous amino acid is selected by H1s, Arg or preferably Va. When the endogenous acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and con-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists. The mutant proteins are also useful in research conditions. Antagonists for a particular GPCRs are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous conditions. Antagonists and AAY90677 and AAY90681-Y90687 the mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to constitutively active, non-endogenous versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 FFMPLGIILECSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL
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52.2%; Pred. No. 2.8e-90;
cive 49; Mismatches 107; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 286-287; 341pp; English.
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                                                                                                                                                                                                                                                                                                                          98US-0170496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Behan DP, Chalmers DT,
                                                                                                                                                                                                                                                                                                                                                                                              (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-329165/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA30738
                                                                                                  WO200022129-A1
Homo sapiens.
                                                                                                                                                                                                                                                                                                                          13-OCT-1998;
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                                                                                                                                                                          20-APR-2000
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                                  Synthetic.
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AAY90637

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Human; G protein-coupled receptor; GPCR; CON103 protein; schizophrenia; neuroleptic; nootropic; neuroprotective; bipolar disease; psychotropic; neurological disorder; psychiatric disease; neurosis; anxiety; neuritis; attention deficit hyperactivity disorder; neurasthenia; senile dementia; affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease, depression; migraine; genetic screening; chromosome 2.
                                                                                                                                                              245 WIVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                            MICLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                   SCCRIEGDIISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL
                                                                                                                                                                                                                                  125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE
                                                                                                                                                                                                                                                                             137 NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE
                                                                                                                                                                                                                                                                                                                             185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL
49; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Transmembrane_domain_(4TM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label = Transmembrane_domain_(5TM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label- Transmembrane_domain_(1TM)
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/note= "First IC loop"
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/note- "Second IC loop"
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/note= "Second EC loop"
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/note- "Third IC loop"
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  Conservative
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258..283
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Matches 178;
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY30673 and AAY30683-Y90697), and to DNA encoding them (AAA30709-A30743 and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X. is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as settings for elucidating the roles for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous constitutions. Antagonist such active, they can be used directly for screening of compounds without the need for endogenous constitutively active, they can be used directly for screening of compounds without the need for endogenous constitutions. The present expresents a human wild-type GPCR referred the constitutions and the constitutively active, they can be used directly for screening of compounds without the need for endogenous constitutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to constitutively active, non-endogenous versions
  Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 880.5; DB 21; Length 387;
Pred. No. 3.6e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                    G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening;
                                                                   300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
                                                                                                              316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
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                                                                                                                                                                                                                                                                                                                                                                           Human G protein-coupled receptor HM74.
                                                                                                                                                                                                                                  AAY90637 standard; Protein; 387 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behan DP, Chalmers DT,
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N-PSDB; AAA30658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agonist; antagonist.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                             21-AUG-2000
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216 ALYLLEFFLPLALILFAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSII 274

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Tue Oct 29 17:01:00 2002
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The invention relates to human G protein-coupled receptor (GPCR) and their corresponding DNA molecules. GPCR is also referred as seven transmembrane receptor. G protein-coupled receptor protein is useful for treating neurological disorder, particularly schizophrenia. GPCR protein is also useful for identifying compounds useful for treating other neurological and psychiatric diseases, e.g. depression, anxiety, bipolar currention deficit disorder, attention deficit hyperactivity disorder, attention deficit disorder, epilepsy, neuritis, neurasthenia, neuropathy, neurosis, Alzheimer's disease, parkinson's disease, migraine and semile dementia. The invention also provides genetic screening procedures that camental analysing a person's genome with respect to GPCR. The vectors are useful for the recombinant production of the GPCR. The present sequence is human CON103 G protein-coupled receptor (GPCR) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seven transmembrane receptor polypeptides and polynucleotides, useful for treating neurological or psychiatric disorders, e.g. schizophrenia, as well as for identifying compounds useful for treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSRASVGAAARVAGGLWVGI-----LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 GPCHPTSSSLVSAFLAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVSADFL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.5%; Score 529; DB 22; Length 384;
39.2%; Pred. No. 1.2e-50;
.ive 48; Mismatches 108; Indels 22;
 /label = Transmembrane_domain_(6TM)
                                                               301..320
/label- Transmembrane_domain_(7TM)
        284.300
/label= Extracellular_domain
/note= "Third EC loop"
301.320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 7-9; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Merchant K;
                                                                                                                                                                                                                                                                                                                                                                                                             (PHAA ) PHARMACIA & UPJOHN CO
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99US-0428020.
99US-0428114.
99US-0429517.
99US-0429555.
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Best Local Similarity 39.28
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood LS,
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                                                                                                                 WO200131014-A2
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28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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27-0CT-1999
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Domain
                                                                   Domain
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This is the amino acid sequence of a novel human G protein coupled receptor, designated HEOAD54, as deduced from a CDNA clone (see AAX06947) isolated from an eosinophil library. A method is claimed for diagnosing susceptibility to disease resulting from mutation of the HEOAD54 gene or imbalance in HEOAD54 polypeptide expression levels. HEOAD54 activate/Inhibit expression, build administration of HEOAD54 activate/Inhibit cosed to prevent expression, while administration of HEOAD54 is used to prevent expression, while administration of HEOAD54 is used to prevent expression, while administration of HEOAD54 is used to treat conditions associated with a lack of HEOAD54 protein. Gene expression. HEOAD54 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, corrects, anorexia, builmia, asthma, Parkinson's disease, acute heart failure, hypotemsion, hypertension, urinary retention, osteoporosis, andian pectoris, myocardial infarction, utcer, allergy, benign prostatic hypertrophy, and psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la
                                                                                                                                                                                                                                                                                        HEOAD54; 7-transmembrane receptor; G protein coupled receptor; signal transduction; human; infection; HIV-1; HIV-2; pain; cancer; anorexia; bulimia; asthma; Parkinson's disease; hypotension; hypertension; acute heart failure; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; anxiety; schlzophrania; delirium; manic demersion; demeria, severe mental reterdation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New G-protein coupled receptor (HEOAD54) polypeptide and polynucleotide - useful as diagnostic reagents, and for prevention and treatment of HIV infections and cancer
238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF
                Sathe GM;
                                                                                                                                                                                                                                                        Human 7-transmembrane receptor HEOAD54.
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                                                                                                                                     AAW88460 standard; Protein; 423
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97US-0060124.
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Fourette's syndrome.

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                                                                                                                                      LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                                                                                                                                                                                                                                                                      124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                201 LSRASVGAAARVAGGLWVGI-----LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
                                                                                                    GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
   ; Pred. No. 1.4e-50;
48; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; G-protein coupled receptor; GPCR; hRUP11; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G-protein coupled receptor, hRUP11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU04365 standard; Protein; 423 AA
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2000US-0181749.
2000US-0189258.
2000US-0189259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0166369.
99US-0171900.
99US-0171901.
39.28;
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2000US-0195899.
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2000US-0203630.
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2000US-0210982.
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2000US-0235418.
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2000US-0242332
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                               Matches 115; Conservative
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N-PSDB; AAS07938.
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200136471-A2.
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12-MAY-2000; 2
12-JUN-2000; 2
12-JUN-2000; 2
21-AUG-2000; 2
26-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1999;
11-FEB-2000;
14-MAR-2000;
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10-APR-2000;
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23-DEC-1999;
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AAU04365
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                                                                                                                                                                                                                                                                         64 LMICLPFRIDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                                                                                                                                                                                                                                                                                                         124, VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: | || : || : || : || 201 LSRASVGAAARVAGGLWVGI-----LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                   4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKFWYFSTVYLFNLAVADFL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein, cDNA and genomic DNA
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                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.5%; Score 529; DB 22; Length 423;
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                                                                                                                                                                     Indels
                                                                                             ; Score 529; DB 20; ; Pred. No. 1.4e-50; 48; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG78785 standard; Protein; 423 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human opioid-type receptor 1.
                                                                                             28.5%;
ilarity 39.2%;
Conservative 4
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(BOEN/) BOENISCH H.
                                                                                                                                   Similarity
                                  423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 AA;
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                                                                                                                                                                  Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG78785;
                                     Sequence
                                                                                                Query Match
Best Local ?
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RESULT 13 AAG7878

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18-MAY-2000
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 7;
                                                                                   hRUP11. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GGCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                     receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; HCSRP; cytostatic; antiarthritic; antirheumatic; antiasthmatic; immunosuppressive; antiarterioscalerotic; antibacterial; antiparasitic; neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia;
                                                                                                                                                                                                                                                                                                                                 64 LMICLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                                                                                                                                                                                                                                                               124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
                                                                                                                                                                                                                                                                                                                                                                                     LSRASVGAAARVAGGLWVGI-----LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 254
                                                                                                                                                                                                                                                                                                                                                                                                           179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
         Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agon
                                                                           sequence represents a human G-protein coupled receptor (GPCR),
                                                                                                                                                                                                                                                                       4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL
                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 FGMASMVAFWLSACRSLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                            Length 423;
                                                                                                                                                                                                                        28.5%; Score 529; DB 22; Length 42
39.2%; Pred. No. 1.4e-50;
Live 48; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's diseases; multiple sclerosis; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141..387
/label- Rhodopsin_GPCR_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128.150
/label- Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..150
te= "Rhodopsin signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cell surface receptor protein #6.
                                                   Claim 13; Page 94-96; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY94339 standard; Protein; 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                Matches 115; Conservative
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159..180
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                   423 AA;
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The present sequence is a novel human cell surface receptor protein (HCSRP) designated HCSRP-6. The nucleotide sequence was identified in correct Clone 2851578 from the CDNA library BRSTTUT13, which was made from the cDNA library BRSTTUT13, which was made from breast tumour tissue. A number of Incyte Clones correct sequence is homologous to rhodopsin-like GPCR/HM7 q21967 isoform g5070877. HCSRP and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRP. Such disorders include cancers such as leukaemia and atherosclerosis, bacterial and parasitic infections and neuronal catherosclerosis, bacterial and parasitic infections and neuronal disorders such as akathesia, Alzheimer's disease, multiple sclerosis and epilepsy. Polynucleotides encoding HSCRPS may be used as hybridisation probes to diagnose these conditions. Anti-HCSRP antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing harmaceutical agents into contact with cells or tissues expressing HCSRP and for Immunogenic fragments are useful for drug screening using libraries of compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human cell surface receptor protein and polynucleotide useful for diagnosis, prevention and treatment of cancer, immune disorders, infection and neuronal disorders
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'note= "Rhodopsin signature"
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Hillman JL, Bandman O, Azimzai Y,
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                                                            "Rhodopsin
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N-PSDB; AAA27049.
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                                                                                    124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
                                                                                                                                                                       179 IMFQLEFFWPLGIILFCSFKIVWSLRRRQQLARQARWKKATRFIMVVAIVFITCYLPSV- 237
                                                                                                                                                                                                               Query Match 28.5%; Score 529; DB 21; Length 455;
Best Local Similarity 39.2%; Pred. No. 1.5e-50;
Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps
                                                                      4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
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TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG 

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541 541 601 601 661

GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG

GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG

421 421 481

361 CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTTGCACCCTGTGG

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The greater inventors to nove to procedure the procedure of the couples at black 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is the coding sequence for one such 6 protein-coupled receptor. Gequence 1s the coding sequence for one such 6 protein-coupled receptor. Getter also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic screening a human to diagnose a disorder affecting the brain or a genetic conferx in a sample is useful for treating schizophrenia. Detection of nGPCRx in a sample is useful for treating schizophrenia. Detection of disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders and hormonal disorders. Modulators of disorders in fections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hypersactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Alacaase) rhammatoid ascentia antitonia disorders include inflammatory conditions (e.g. Crohn's antitonia disorders).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory allments such as asthma, and inflammatory diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to novel G protein-coupled receptors
                                                                                                                                                                                                                                                                                                                                                                   nd P, Slightom J;
Sejlitz T, Huff
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PS, Bannigan CM, Ruff V,
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Pred. No. 4e-288;
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Matches 1041; Conservative
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09-MAR-2000;
17-MAR-2000;
               17-NOV-1999;
19-NOV-1999;
28-DEC-1999;
22-FEB-2000;
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02-MAR-2000;
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Human GPCRla polynucleotide SEQ ID NO 1.
                                           ABA81529 standard; DNA; 1050 BP
                                                                                      (first entry)
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                                 ABA81529
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                                                                         GATTICCICCTIAIGAICIGCCIGCCITITICGGACAGACIAITACCICAGACGIAGACAC 240
                                                             CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTTTC 120
                                                                                                      TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180
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anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
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CACATTGTTGAGTGGCACTGA 1041
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TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAAATCTGCAGTCTGAAACCCAAG

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CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG

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TICATCATGGTGGTGGCAATTGTGTTCATCATGCTACCTGCCCAGCGTGTCTGCTAGA 

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721 721 781 781

CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT

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CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC

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245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
                                                                                                                                                                                                                                                                                                                                                                                                       185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
                                                                                                                                                                                                                                                                     65 MICLPFRIDYYLRRHWAFGDIPCRVGLFILAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                                                                                                                                                                                                                                                                                     NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
                                                                                                                                                                                                                        5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
               manic depression, depression, delirium, dementia, and severe me retardation, and dyskinesias such as Huntington's disease or Gilles de la Tourett's syndrome. The products can also be used detection, diagnosis and drug screening.
                                                                                                                                                                  47; Mismatches 107; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
                                                                                                                                  47.7%; Score 883.5; DB 2
52.8%; Pred. No. 1.5e-90;
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lung cancer.
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                                                                                                                                                    Similarity
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11-FEB-2000;
14-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension;
                                                                                                                                                WAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLW 140
                                                                                                                                                                                               ALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLEFFMPLGIILFCSFKIV 200
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                                                            LLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRH 80
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             Pred. No. 6.8e-168;
Mismatches 0;
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100.08; Fr. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US12386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                             Conservative
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               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX16671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9856820-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-1998;
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                             296;
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2000US-0200419 0000S-0203630 2000US-0210982

28-APR-2000;

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AAH51053 standard; DNA; 24 BP.

RESULT 15 AAH51053 (first entry)

28-AUG-2001

AAH51053;

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The present sequence encodes a member of the G-protein coupled receptor (7TM receptor) family, designated the HM74A receptor. The proteins, agonists, antagonists and polynuclectides can be used for treating disorders associated with increased or reduced expression or activity of HM74A, e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, clabetes, obbesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, mycoardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, maint depression, depression, delinium, dementia, and severe mental retardation, and dyskinesias such as Huntington's disease or cities de la Tourett's syndrome. The products can also be used for
                                                                                                                                                                                                                                            HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension; asthma; allergy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated G-protein coupled receptor, HM74A - used to develop products for treating e.g. infections, pain, cancers, diabetes, obesity, neurological disorders, heart failure, hypertension, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mooney JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1361;
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Score 32; DB 20; Lengu...
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0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li X,
                                                                                                                                                                                                               G-protein coupled receptor HM74A encoding cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                 /product- "HM74A receptor"
               838 CTCAGCTTCACCTACATGAACAGCATGCTGGA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection, diagnosis and drug screening
790 CTCAGCTTCACCTACATGAACAGCATGCTGGA
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
61..1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 30-31; 40pp; English.
                                                                                                            AAX16671 standard; cDNA; 1361 BP
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P-PSDB; AAW94654.
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The present invention relates to novel G protein-coupled receptors (GPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see CRH50969-AAH51015 and AAH51010S and AAG80929-AAG80975 and AAG80977). The present sequence is an oligonucleotide, which was used in the present present sequence as an oligonucleotide, which was used in the present invention of GPCRs are also known as seven transmembrane receptors and invention in signal transduction. The nGPCRx coding sequences are useful consciount of a present predisposition, specifically schizophrenia. nGPCRx are useful conferent in a sample is useful for treating schizophrenia. Detection of GPCR in tentifying compounds useful for treating schizophrenia. Detection of GPCRX disorders e.g. thyroid disorders, remain failure, rheumatoid arthritis, clisorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of
                                                                                                              G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit thyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parodi LA, Hiebsch RR, Lind P, Slightom J;
PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating \varepsilon,g . schlzophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 246; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA & UPJOHN CO
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99US-0166678.
99US-0173396.
2000US-0184129.
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25-MAY-2000; 2000US-0207094.
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2000US-0188114.
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                                                                                  Oligonuclectide SEQ ID 133.
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                                                                                                                                                                                                                                                                 neuroprotective; ss.
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20-APR-2000;
02-MAY-2000;
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03-MAR-2000;
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790 CTCAGCTTCACCTACATGAACAGCATGCTGGA 821

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Query Match Best Local Similarity 100. Matches 32; Conservative

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